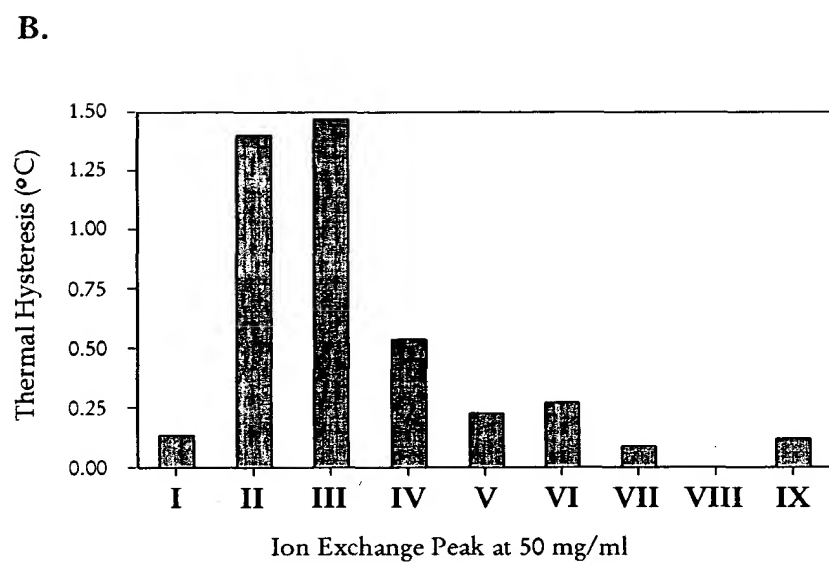
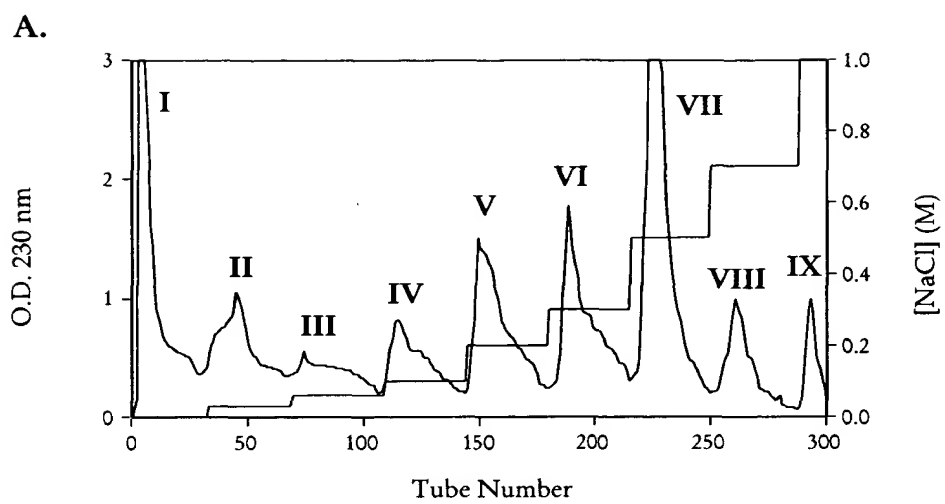
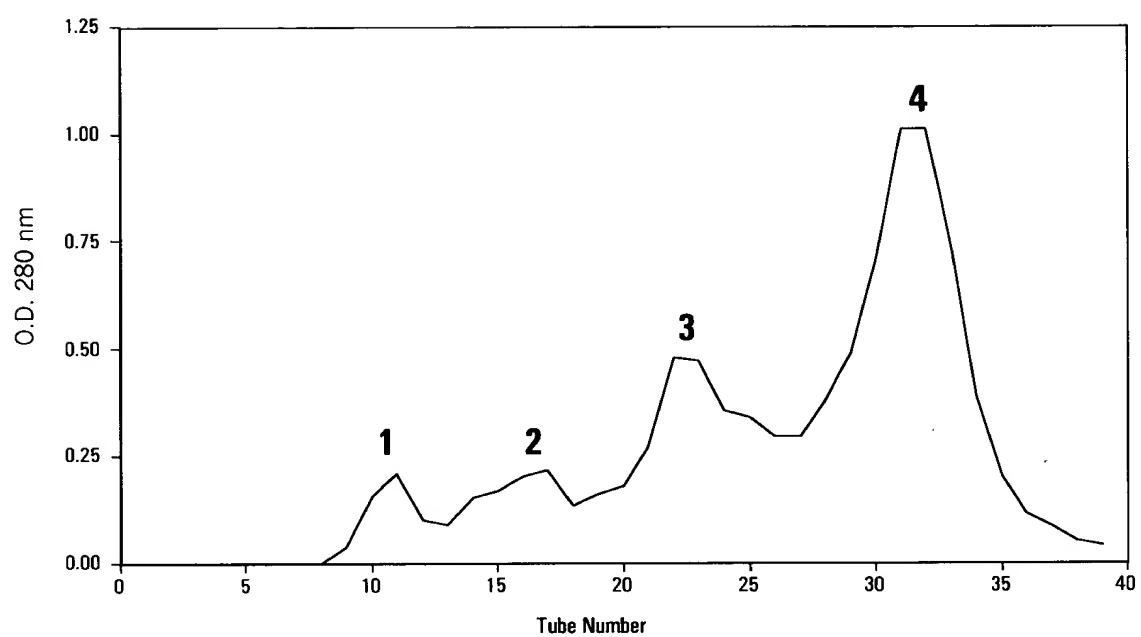


Fig. 1.0

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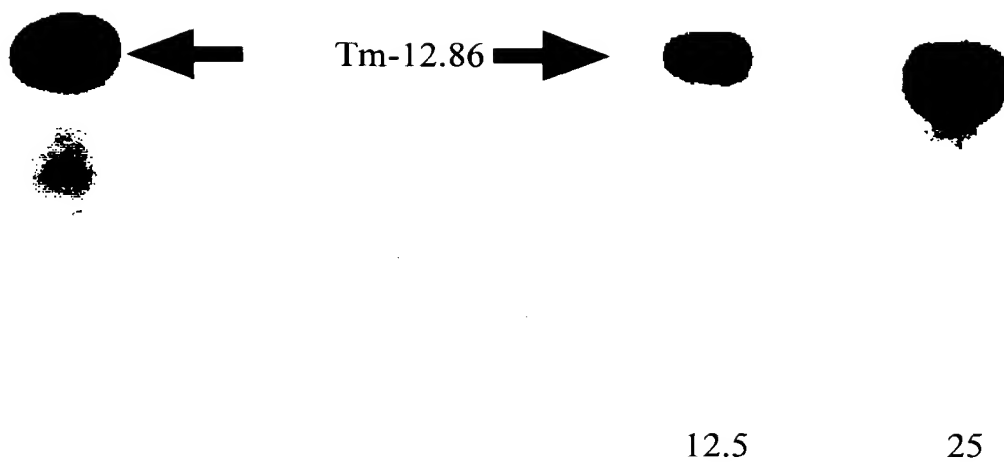


*Fig. 1.1*

[illegible]

*Fig. 1.2*

090796-0400

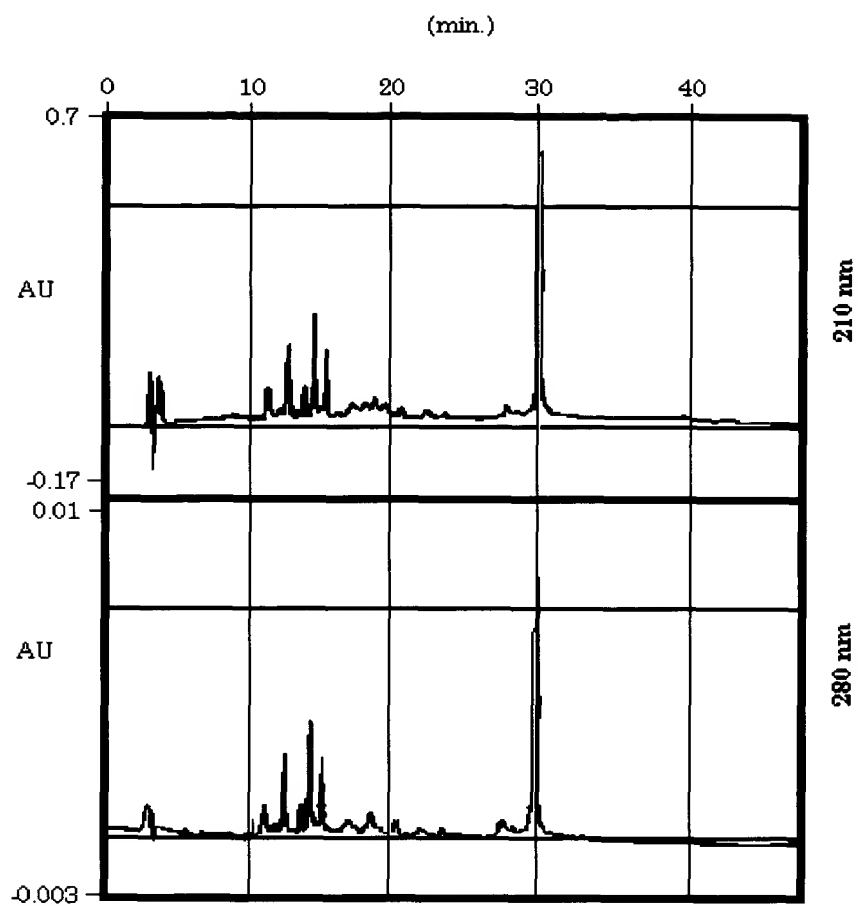


*Fig. 1.3*

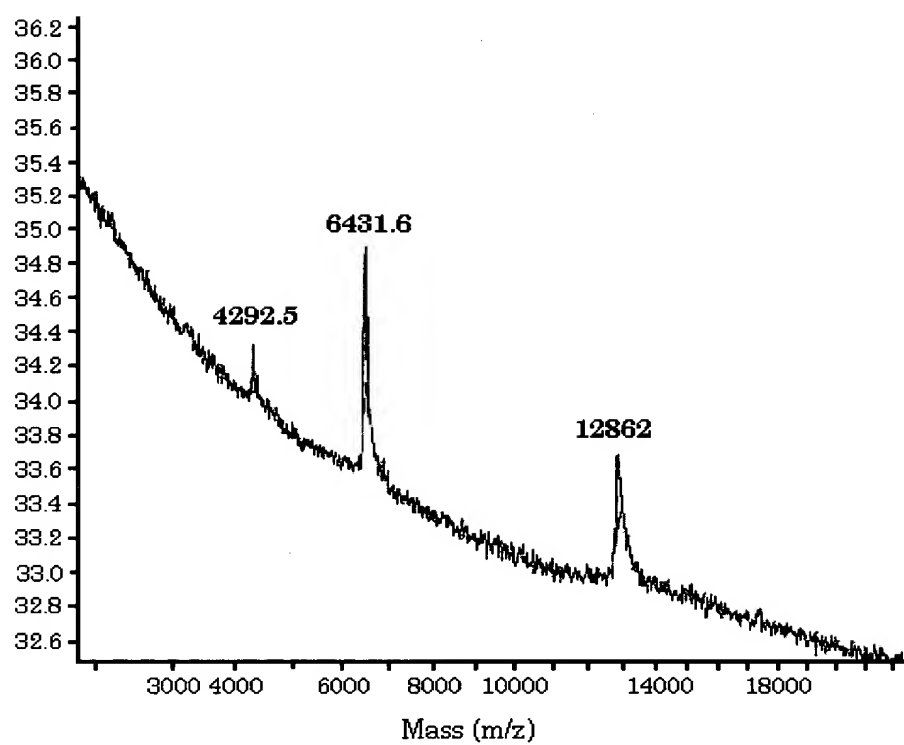
*Fig. 1.4*



202120 95292860

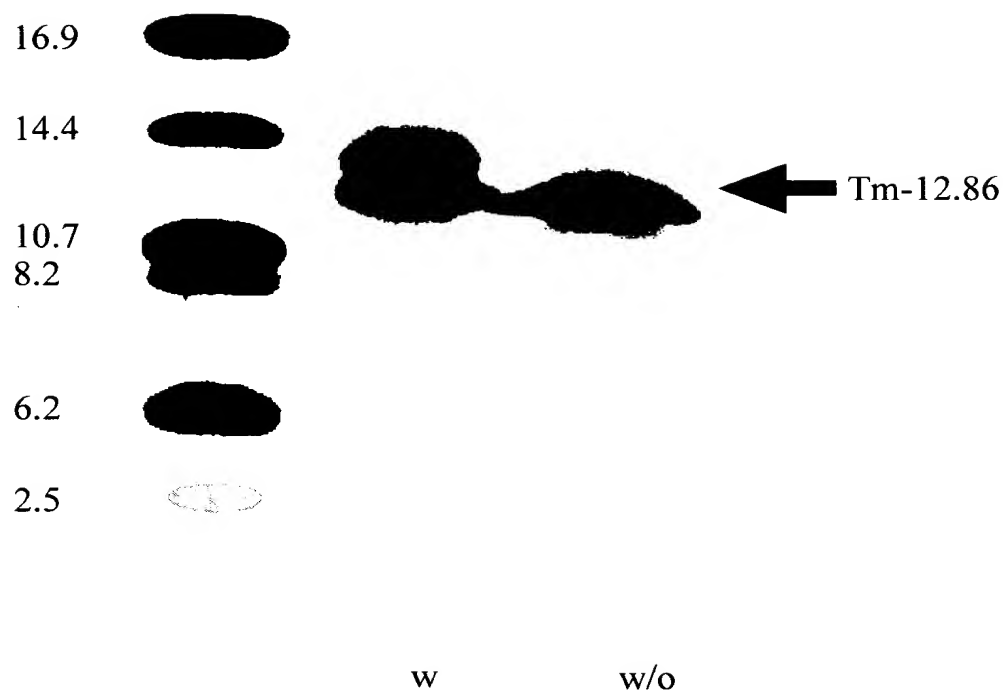


*Fig. 1.5*



*Fig. 1.6*

2021.09.23.09.50.00



*Fig. 1.7*

**NH<sub>2</sub>-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V**  
 Leu Thr Asp Gln Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Gln Gln Val

*Fig. 1.8*

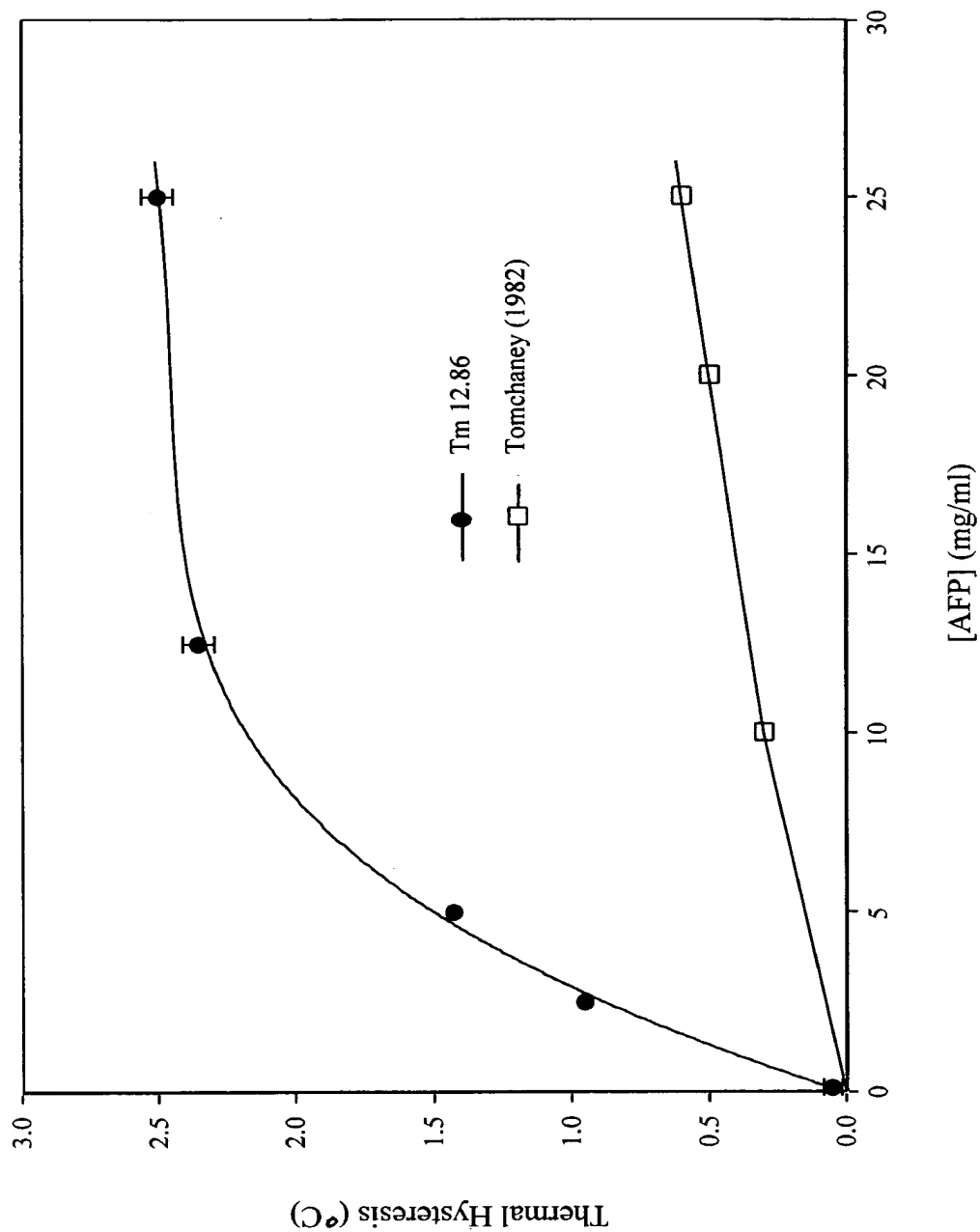
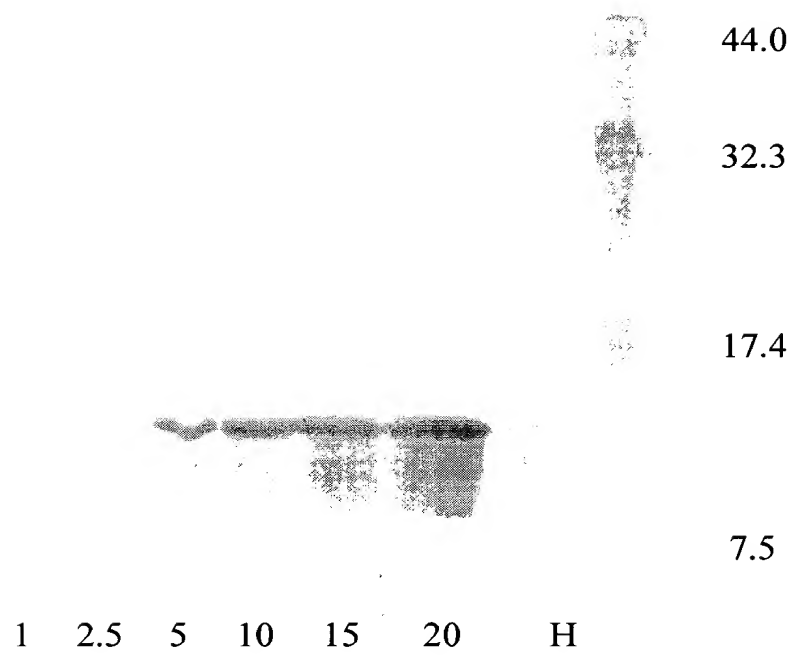
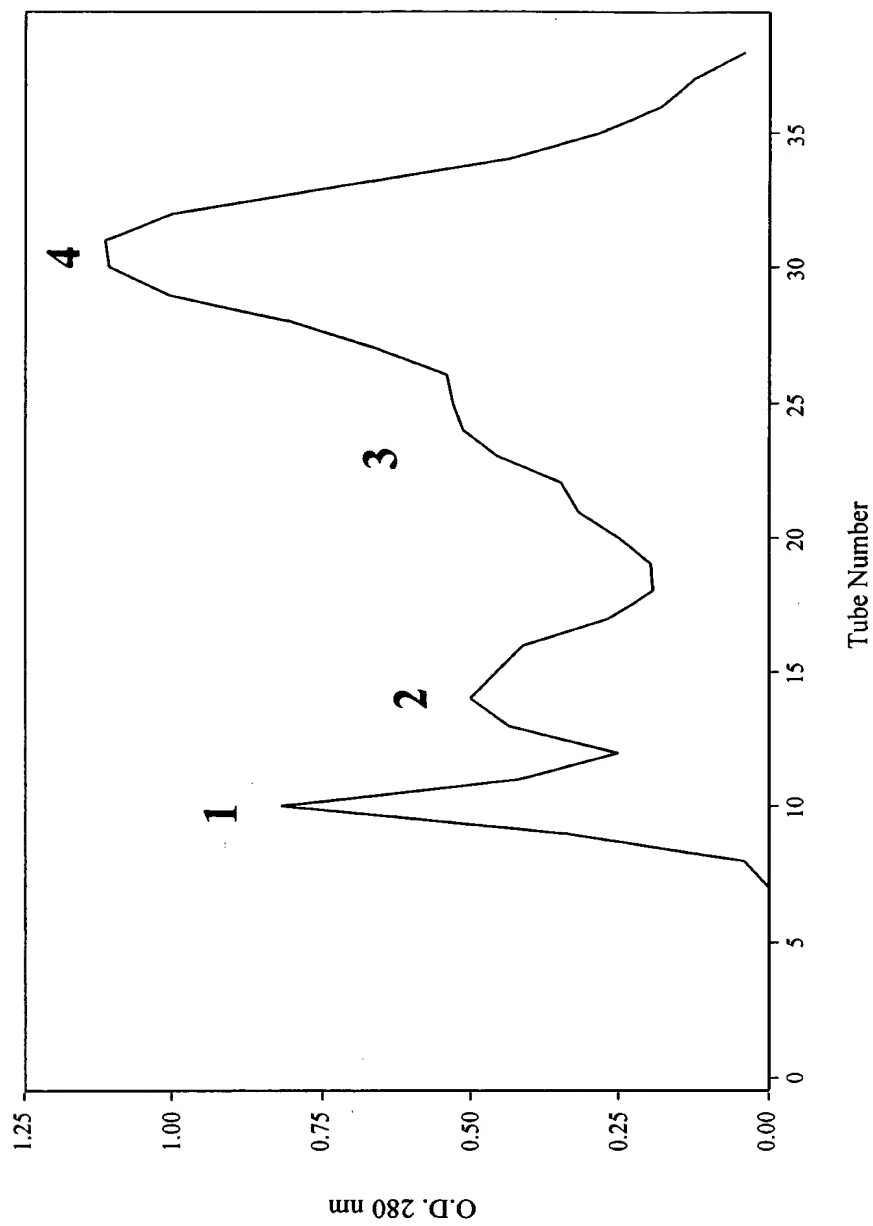


Fig. 1.9

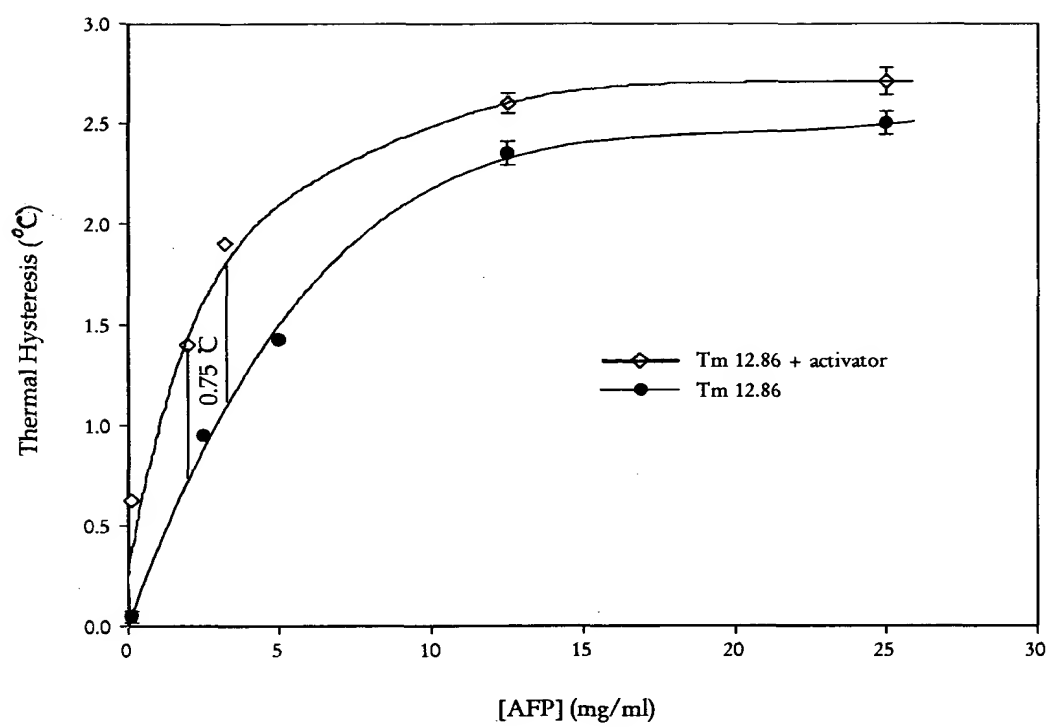


*Fig. 1.10*

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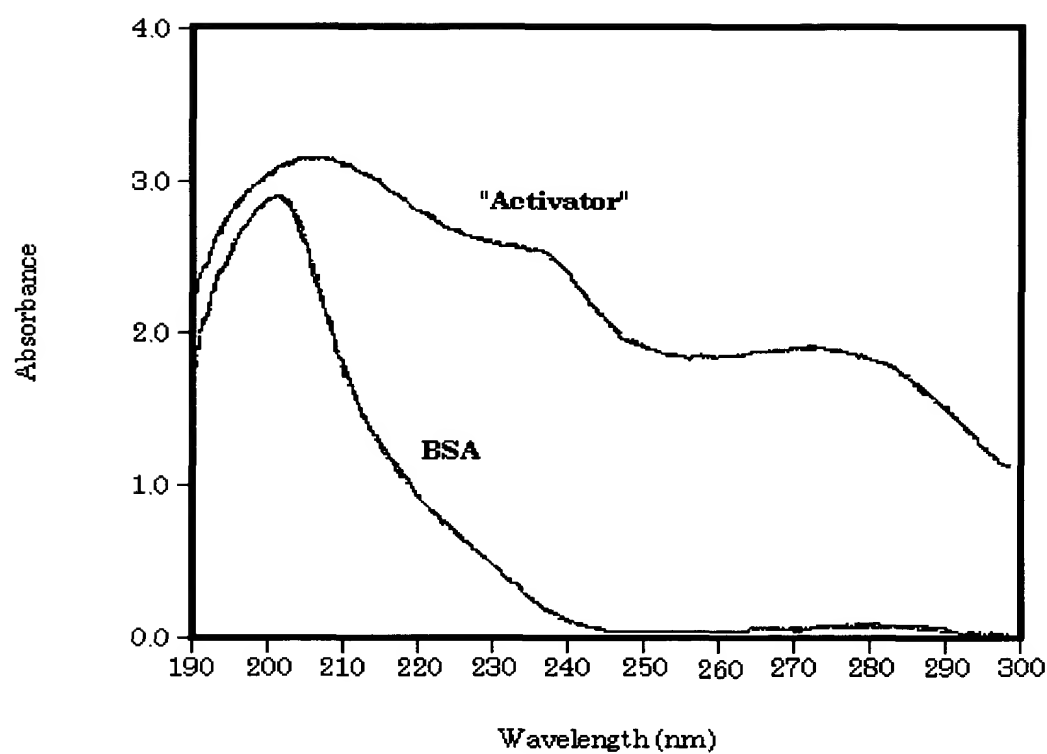


*Fig. 1.11*



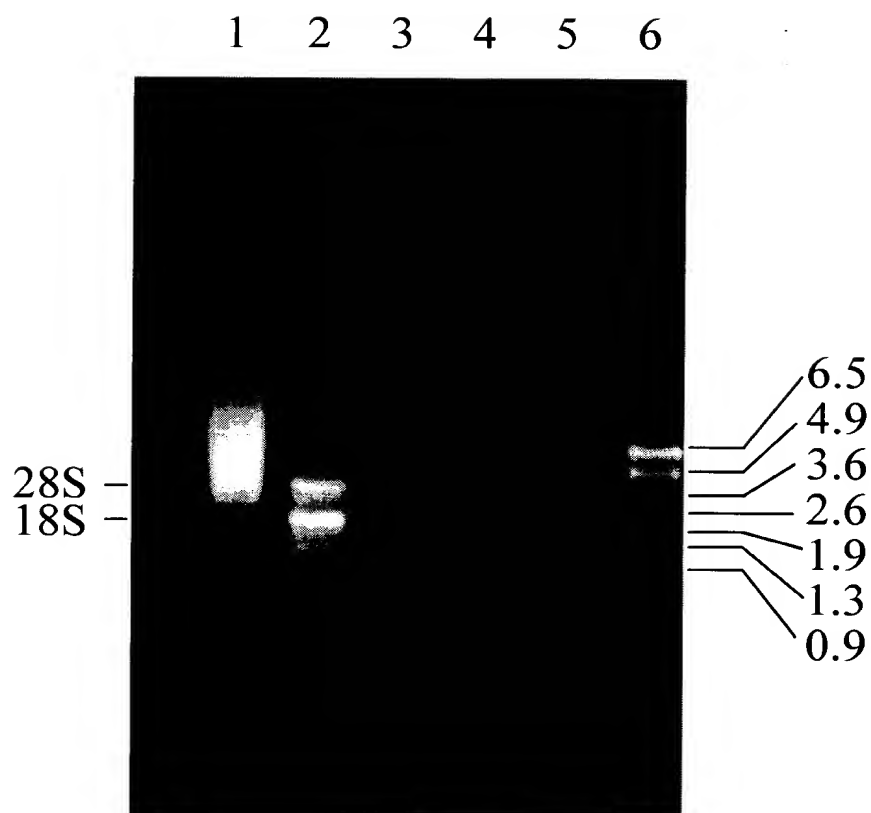
*Fig. 1.12*



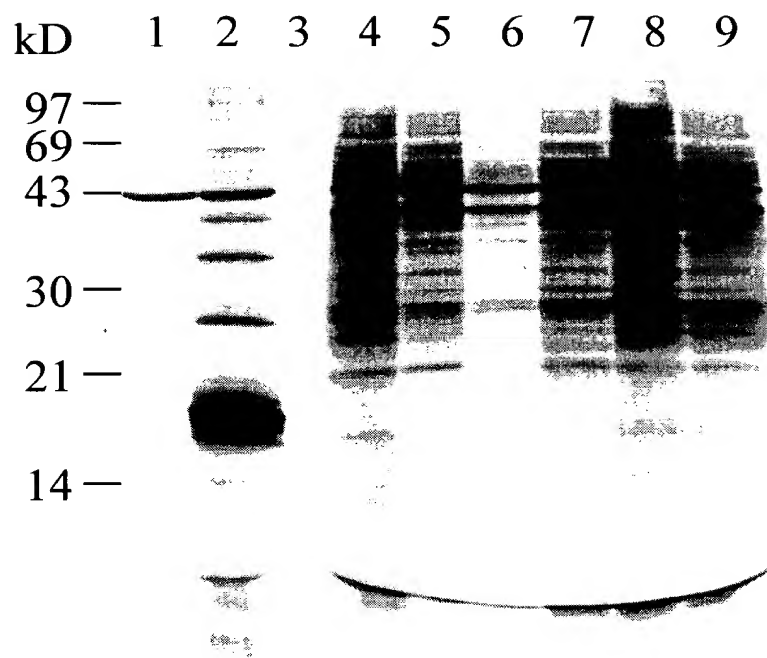


*Fig. 1.13*

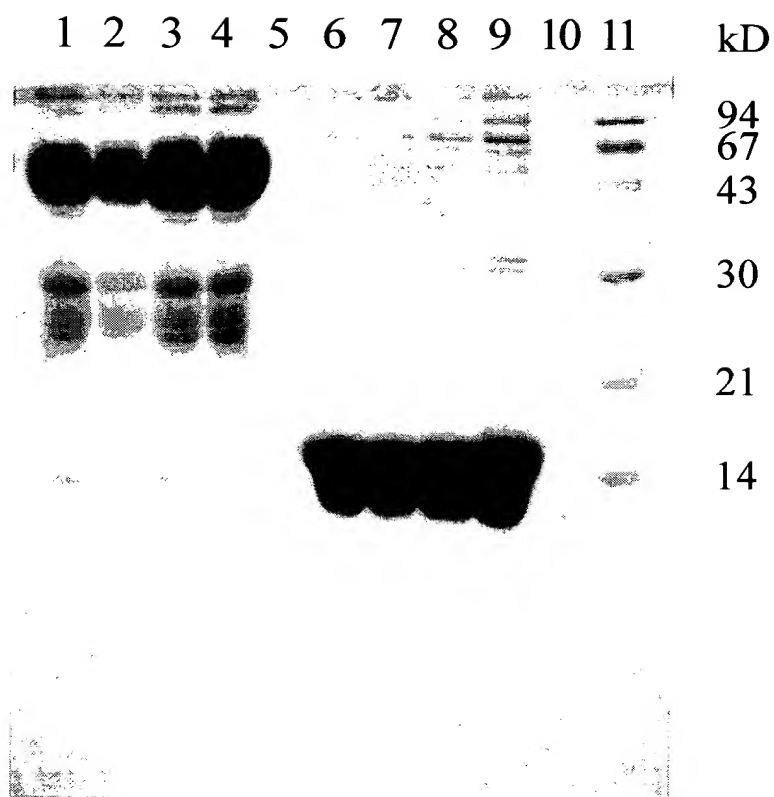
28S  
18S



*Fig. 2.0*



*Fig. 2.1*



*Fig. 2.2*

1 2 3 4 5 6 7 8 9 kD



*Fig. 2.3*

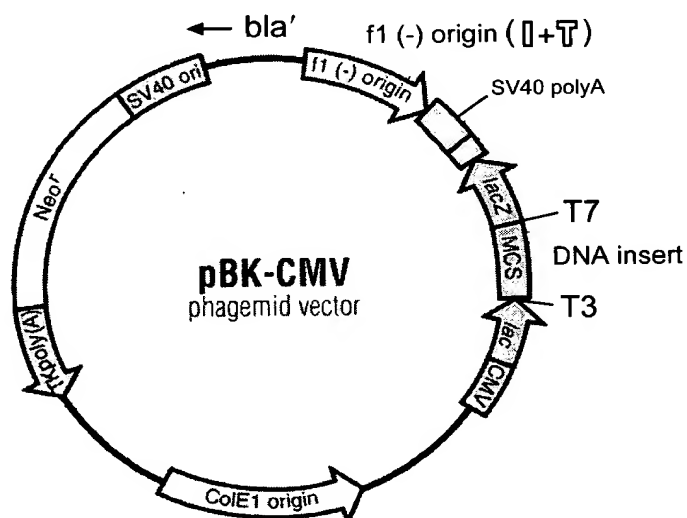
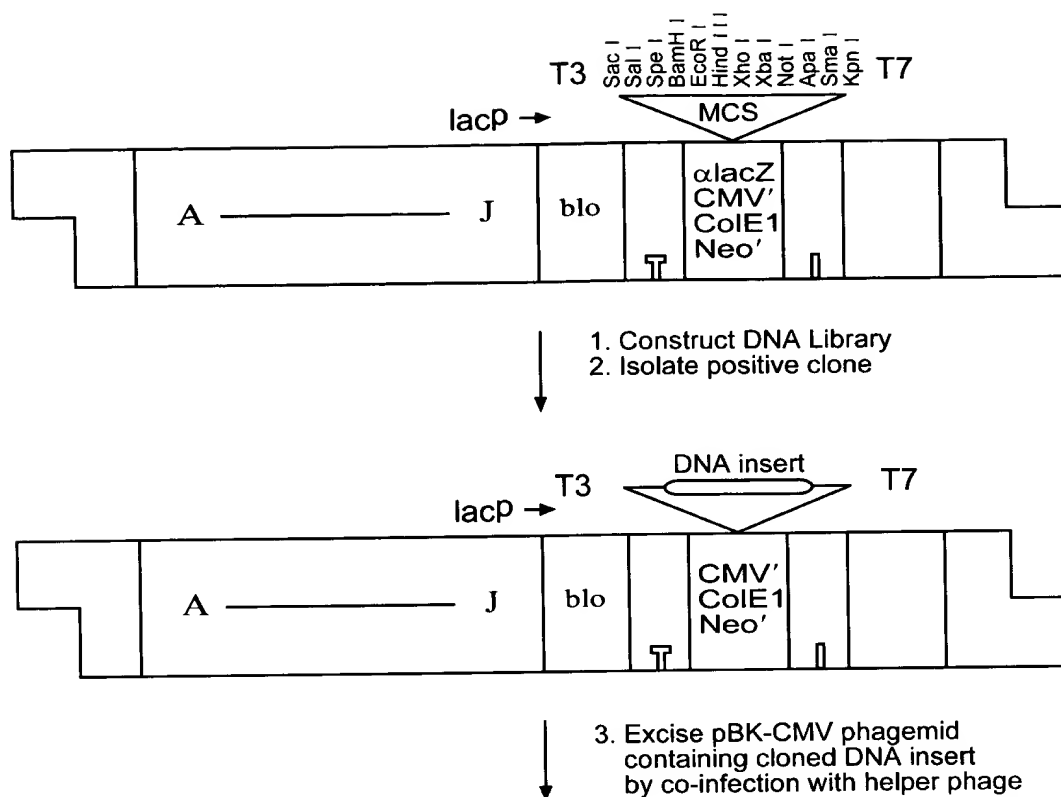
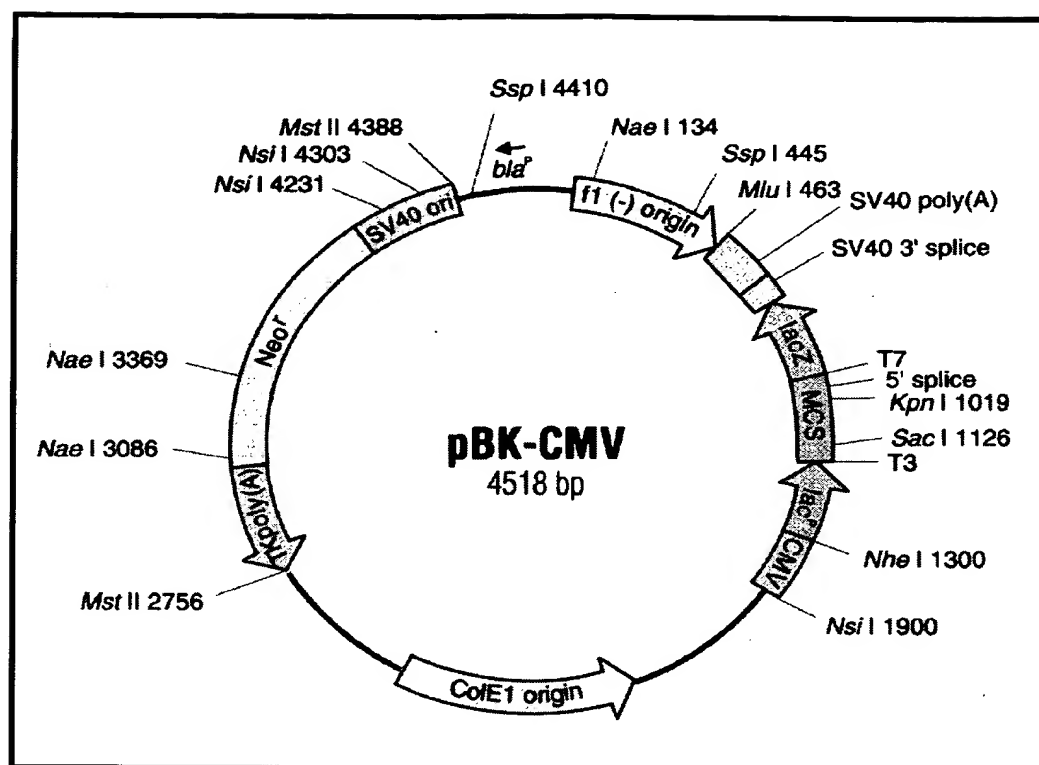
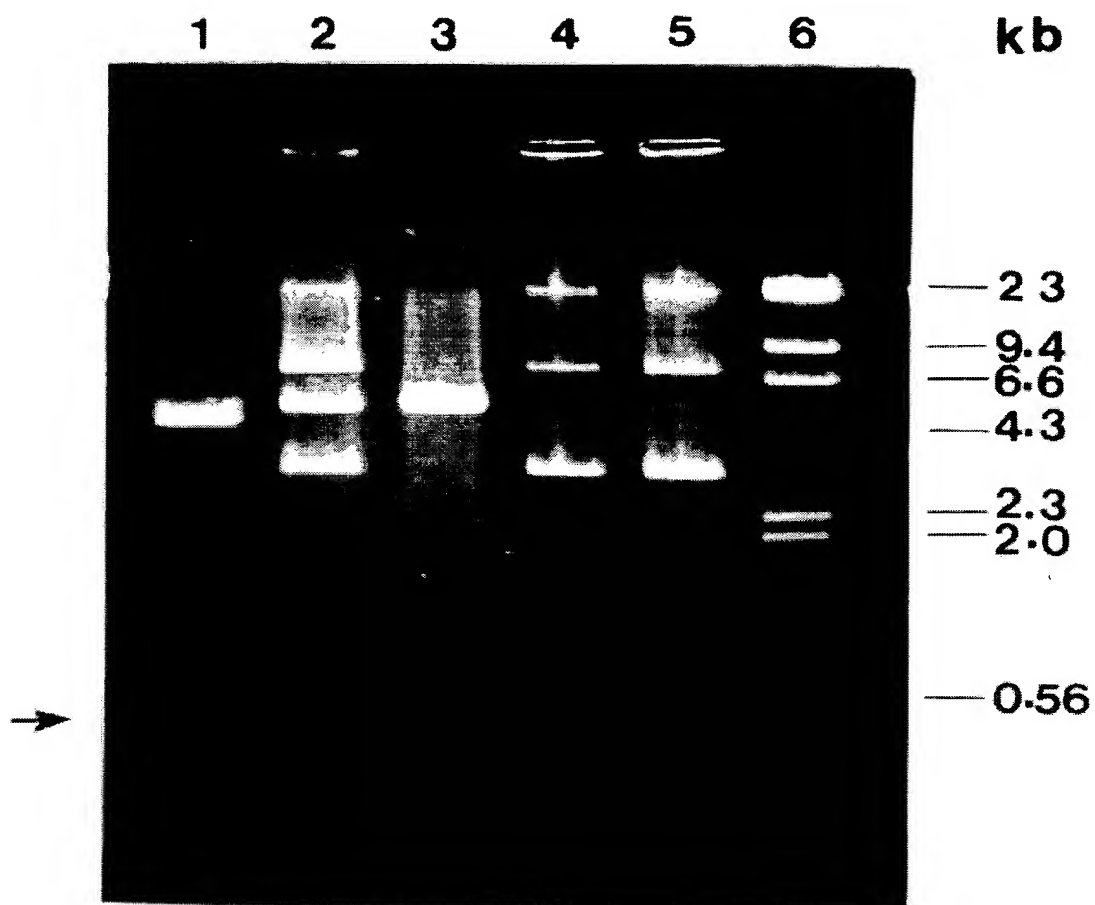


Fig. 2.4a



BK Reverse Primer 5' ACAGGAACAGCTATGACCTTG 3'  
 T3 Primer 5' AATTAACCCCTCACTAAAGGG 3'  
 T3 promoter +1 →  
 1200 MET  
 5' TCACACAGGAACAGCTATGACCTTGATTACGCCAAGCTCGAAATTAACCTCACTAAAGGGAAACAAAGCTGGAGCTCGCGCCCTGCAGGTCGACACTAGTGGATCCAAAG  
 3' AGTGTCCTTTTGTGATACTGGAACATAATGCGGTTTCGACCTTTAATTGGGAGTGATTCCTTGTTTTTCGACCTCGAGCGCGGGAGCTCCAGCTGTGATCACTAGGTTTCTTAA  
 1183 β-Galactosidase →  
 Xho I  
 Hinf I Sca I Xba I Not I Apa I Cla I Asp106 I BstX I Sma I Kpn I  
 AATCAAAAAGCTTCTCGAGAGTACTTCTAGAGCGGCCGCGGCCCATCGATTTTCCACCGGGTGGGGTACCAGGTAAGTGTACCCAAATTCGCCCTATAGTGAATCGTATTACAATTCACCTGGCCGTCGTTTACA 3' (+)  
 GTTTTTCGAAGAGCTCTCATGAAGATCTCGCGGCCGCCGGGTAGCTAAAAGGTGGGCCCAECCATGGTCCATTACATGGGTTAAGCGGGATATCACTACACATAATGTTAAGTGACCGGAGCAAAATGT 5' (-)  
 ← +1 T7 promoter 961  
 3' CGGGATATCACTCAGCATAATG 5' 3' TGACCGGACGCAAAATG 5'  
 T7 Primer H13-20 Primer

Fig 2.46



*Fig. 2.5*



# DNA sequence of Tm 13.17 cDNA clone

B E  
 a c  
 m o  
 H R  
 I I

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGTGAAGTTGCTCTGTTGTCTAATCT  
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA  
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAGCTC  
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA  
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA  
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCCTGTCGCAAGA  
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA  
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC  
 F S P V D \*

481 ATATAAAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG  
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTCCACCC

X  
 h  
 o  
 I

Fig. 2.6a

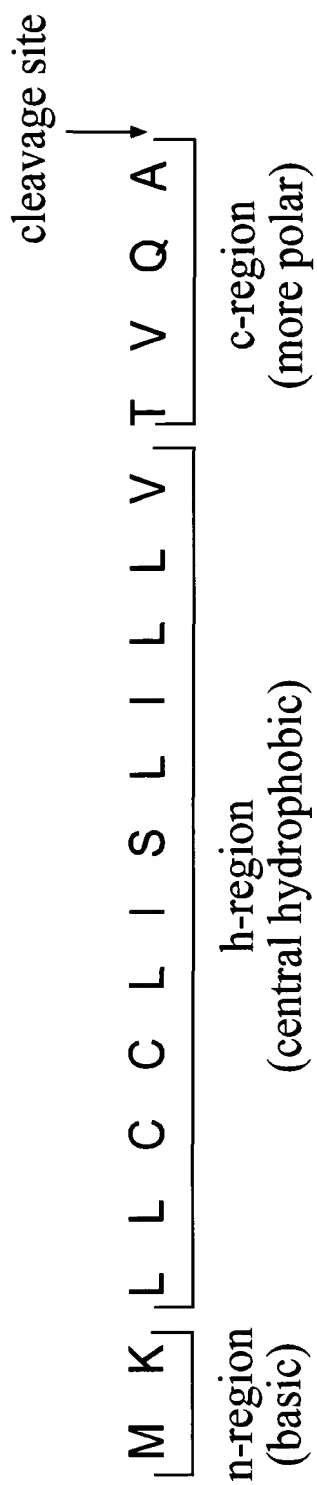


Fig. 2.6b

**A. Mature Tm 13.17 amino acid residue**

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RRGDWEDDPK LKRQVFCVAR  
 51 NAGLATESGE VVVDVLRKV RKVTDNDEET EKIINKCAVK RDTVEETVFN  
 101 TFKCVMKNKP KFSPVD

**B. Summary of the composition analysis for the mature Tm 13.17 sequence:**

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = <b>Glu</b>	<b>13</b>	<b>11.207</b>
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = <b>Lys</b>	<b>16</b>	<b>13.793</b>
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = <b>Val</b>	<b>14</b>	<b>12.069</b>
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

*Fig. 2.6c*

[illegible]

*Fig. 2.7*

Tm 13.17	3	EAQIEKLNKISKKCQNESGVSEIITKARNGDWEDDPKLKRQVFCVARNA	52
		..    ..  .  ..   :  :. .   :       :.  : ..	
AFP-3	1	ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAF CILKRA	50
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTNDDEETEKIINKCAVKRDTVEETVFNTF	102
		: ..   . :  :.. .. :.. .....     :   ..... :	
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFF	100
Tm 13.17	103	KCVMKNKP	110
		. :.	
AFP-3	101	KCVHDNRS	108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

*Fig. 2.8*

Tm 13.17	M	K	L	L	C	C	L	I	S	L	I	L	V	T	V	Q	A
AFP-3	M	K	L	L	L	C	L	V	L	V	A	L	V	A	T	Y	A
B Protein				L	T	S	L	I	L	L	V	A	V	Q	A		

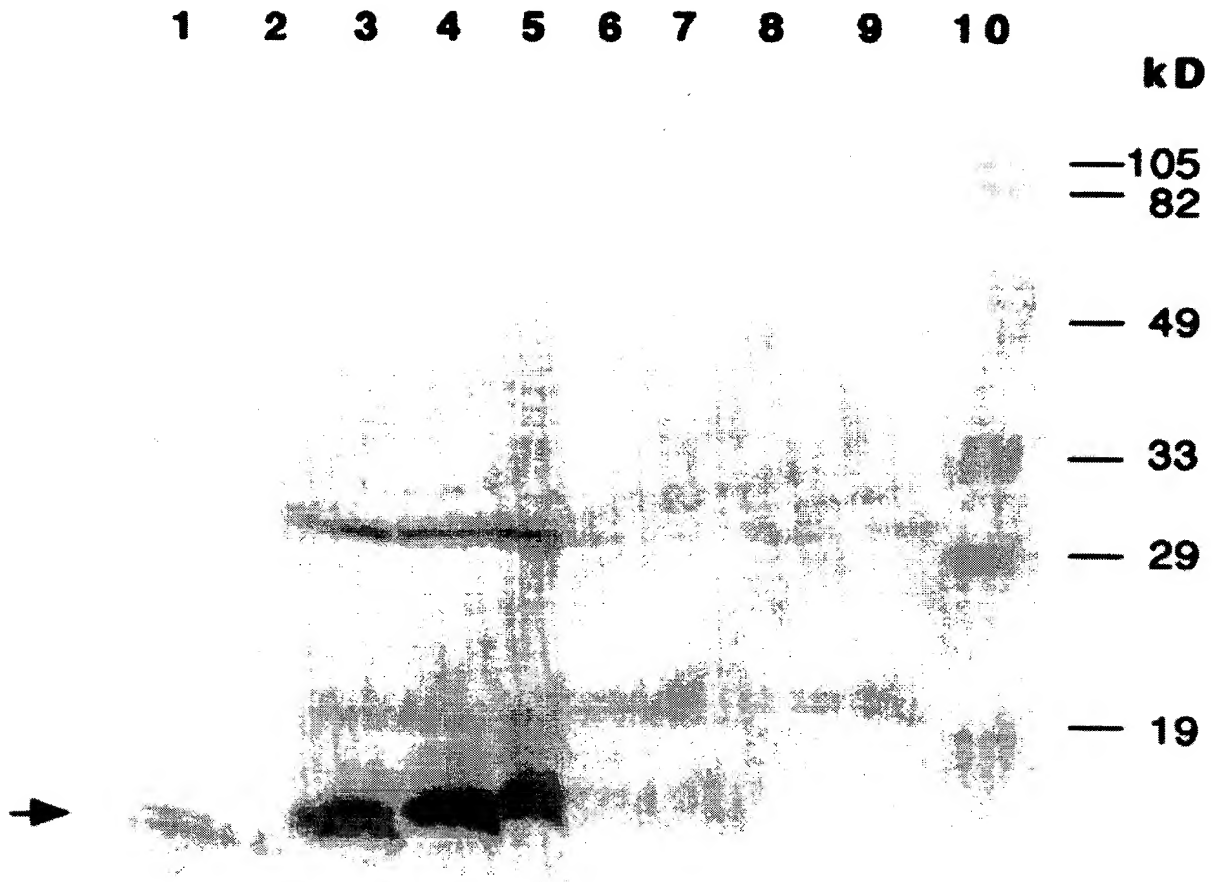
Fig. 2.9

Tm 13.17	NH2	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E
Tm 12.86	NH2	L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V

*Fig 2.10*

202420" 05/07/86

202720" 06292060



*Fig 2.11*



Tm 12.86		L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V											
Tm 13.17	1	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E	S	G	V	S	Q	E	I	I	T	K	A
B1	13	I	T	E	E	D	L	E	L	L	R	Q	T	S	A	E	C	K	T	E	S	G	V	S	E	D	V	I	K	R	A
AFP-3	1		E	T	P	R	E	K	L	K	Q	H	S	D	A	C	K	A	E	S	G	V	S	E	E	S	L	N	K	V	
Tm13.17	31	R	N	G	D	W	E	D	D	P	K	L	K	R	Q	V	F	C	V	A	R	N	A	G	L	A	T	E	S	G	E
B1	44	R	K	G	D	L	E	D	D	P	K	L	K	M	Q	L	L	C	I	F	K	A	L	E	I	V	A	E	S	G	E
AFP-3	29	R	N	R	E	E	V	D	D	P	K	L	K	E	H	A	F	C	I	L	K	R	A	G	F	I	D	A	S	G	E
Tm13.17	61	V	V	V	D	V	L	R	E	K	V	R	K	V	T	D	N	D	E	E	T	E	K	I	I	N	K	C	A	V	K
B1	75	I	E	A	D	T	F	K	E	K	L	T	R	V	T	N	D	D	E	E	S	E	K	I	V	E	K	C	T	V	T
AFP-3	59	F	Q	L	D	H	I	K	T	K	F	K	E	N	S	E	H	P	E	K	V	D	D	L	V	A	K	C	A	V	K
Tm13.17	91	R	D	T	V	E	E	T	V	F	N	T	F	K	C	V	M	K	N	K	P	K	F	S	P	V	D				
B1	106	E	D	T	P	E	D	T	A	F	E	V	T	K	C	V	L	K	D	K	P	N	F	F	G	D	L	F	V		
AFP-3	89	K	D	T	P	Q	H	S	S	A	D	F	F	K	C	V	H	D	N	R	S										

Fig. 2.12

1    GGCACGAGCAAAA ATG AAACTCCTCTTGTGCTTTGCGTTTCGCCGCC  
                                  M   K   L   L   L   C   F   A   F   A   A  
 47    ATCGTCATCGGAGCTCAGGCTCTCACCAGACGAACAGATACAGAAA  
          I   V   I   G   A   Q   A   L   T   D   E   Q   I   Q   K  
 92    AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC  
          R   N   K   I   S   K   E   C   Q   Q   V   S   G   V   S  
 137    CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT  
          Q   E   T   I   D   K   V   R   T   G   V   L   V   D   D  
 182    CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA  
          P   K   M   K   K   H   V   L   C   F   S   K   K   T   G  
 226    GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
          V   A   T   E   A   G   D   T   N   V   E   V   L   K   A  
 271    AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG  
          K   L   K   H   V   A   S   D   E   E   V   D   K   I   V  
 316    CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT  
          Q   K   C   V   V   K   K   A   T   P   E   E   T   A   Y  
 361    GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT  
          D   T   F   K   C   I   Y   D   S   K   P   D   F   S   P  
 406    ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT  
          I   D  
    polyadenylation signal  
 451    ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

poly (A) tail

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC  
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA  
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC  
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT  
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA  
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG  
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT  
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT  
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT  
I D

polyadenylation signal

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAA

poly (A) tail

Fig 3.1

Start  
↓

2-2	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C <span style="border: 1px solid black;">G</span>
2-3	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C <span style="border: 1px solid black;">T</span>
2-2	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-3	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-2	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-3	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-2	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-3	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-2	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A <span style="border: 1px solid black;">T</span> G A T C C C A
2-3	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A <span style="border: 1px solid black;">C</span> G A T C C C A
2-2	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
2-3	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
2-2	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
2-3	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
2-2	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-3	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-2	A A G A <span style="border: 1px solid black;">G</span> G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-3	A A G A <span style="border: 1px solid black;">A</span> G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-2	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-3	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-2	A A G T G T A T T T A C G A C A G <span style="border: 1px solid black;">C</span> A A A C C T G A T T T C T C T C C T A
2-3	A A G T G T A T T T A C G A C A G <span style="border: 1px solid black;">T</span> A A A C C T G A T T T C T C T C C T A
2-2	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
2-3	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
2-2	T A A A G G T A <span style="border: 1px solid black;">A</span> T A T C G T T A T G <span style="border: 1px solid black;">T</span> A A A A A
2-3	T A A A G G T A <span style="border: 1px solid black;">C</span> T A T C G T T A T G <span style="border: 1px solid black;">A</span> A A A A A

*Fig 3.2*

## Predicted Amino Acid

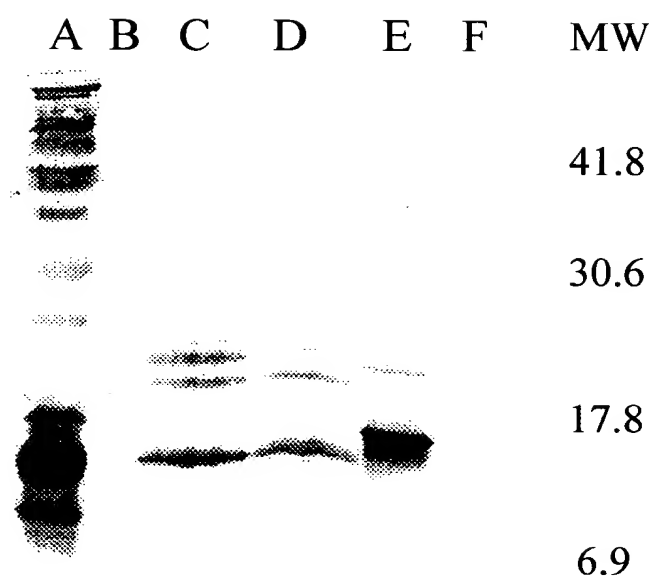
### Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

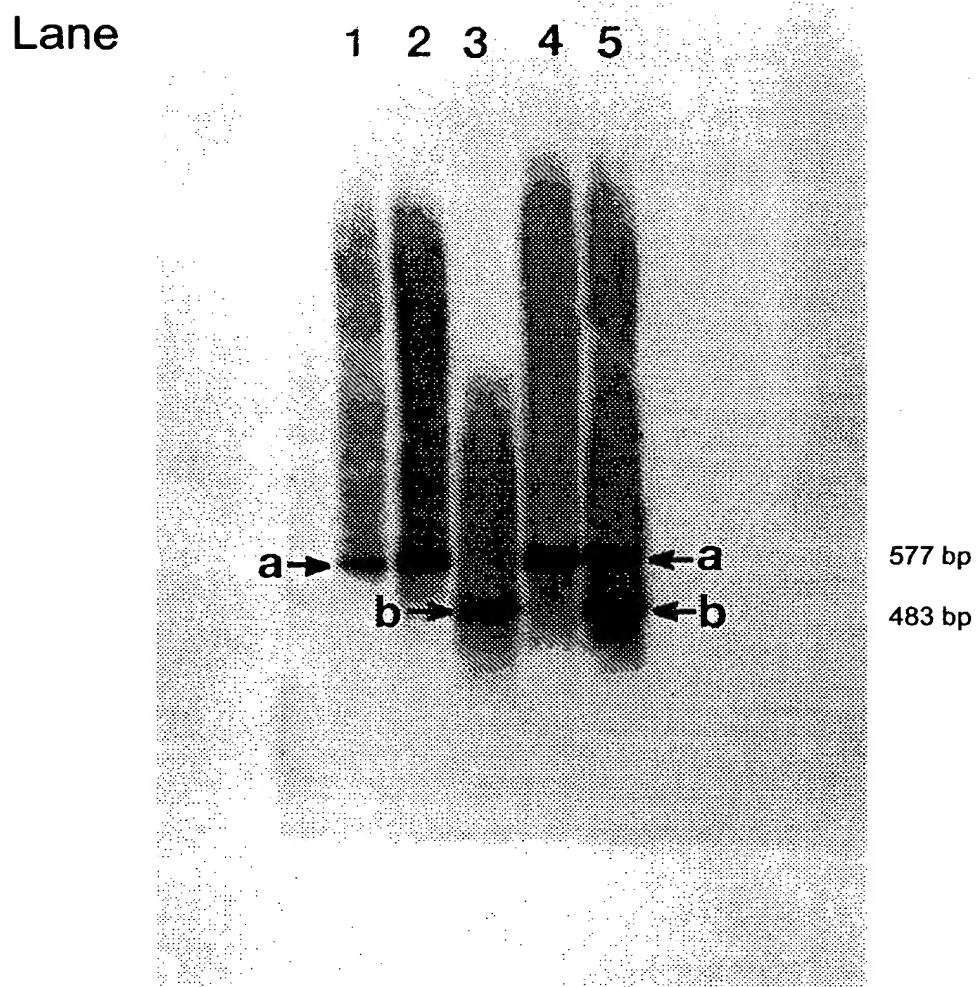
#### Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

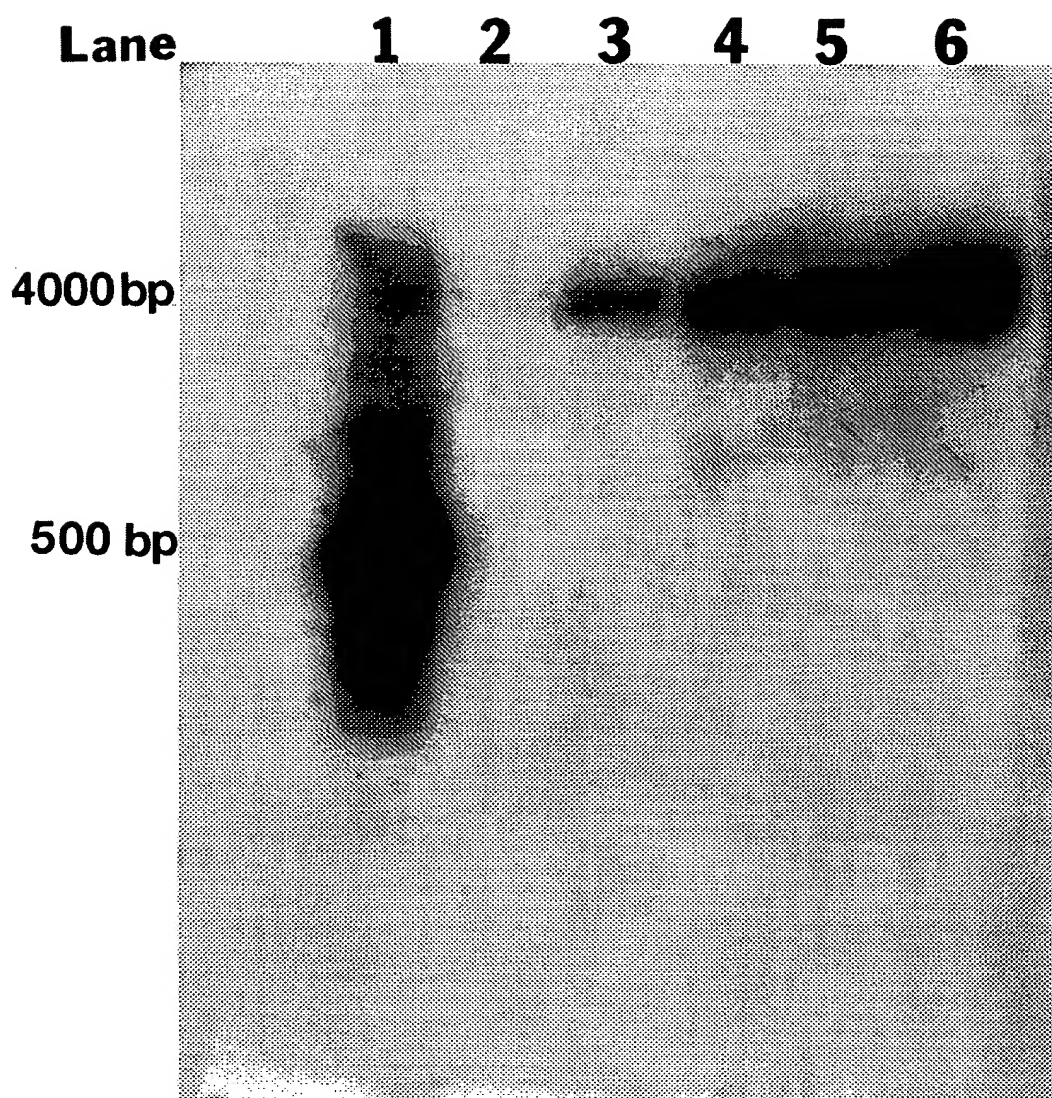
*Fig. 3.3*



*Fig. 3.4*

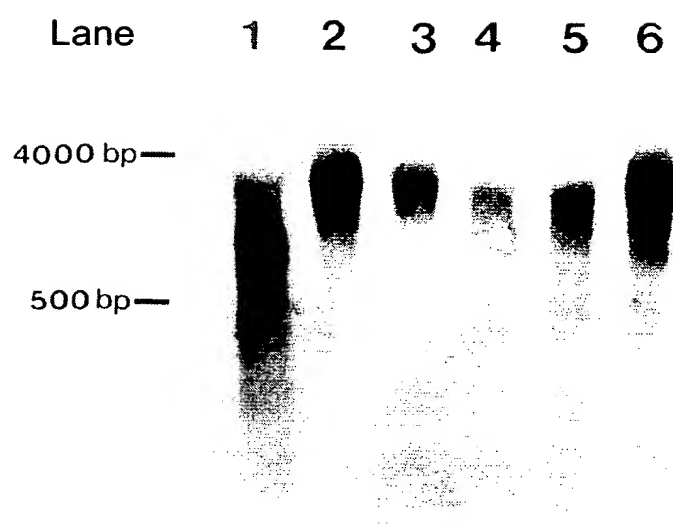


*Fig. 4.0*



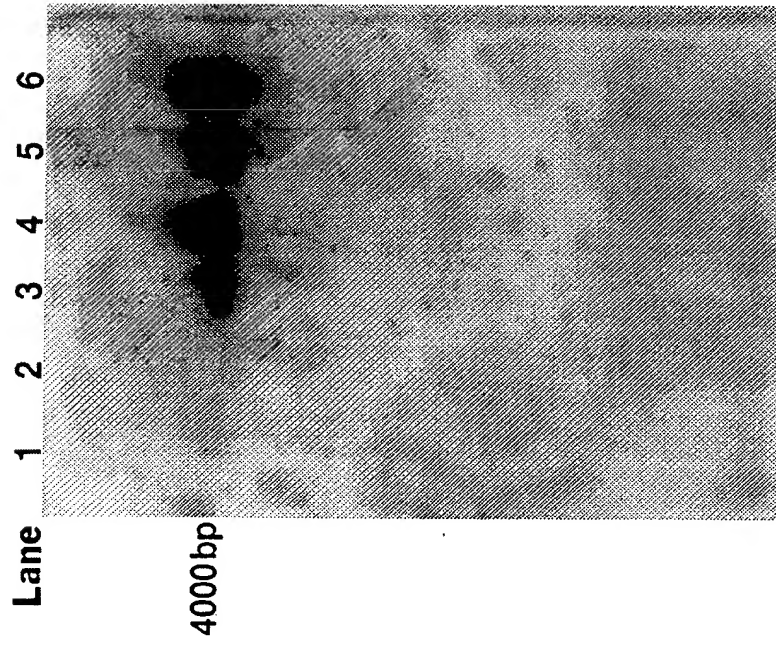
*Fig. 4.1*



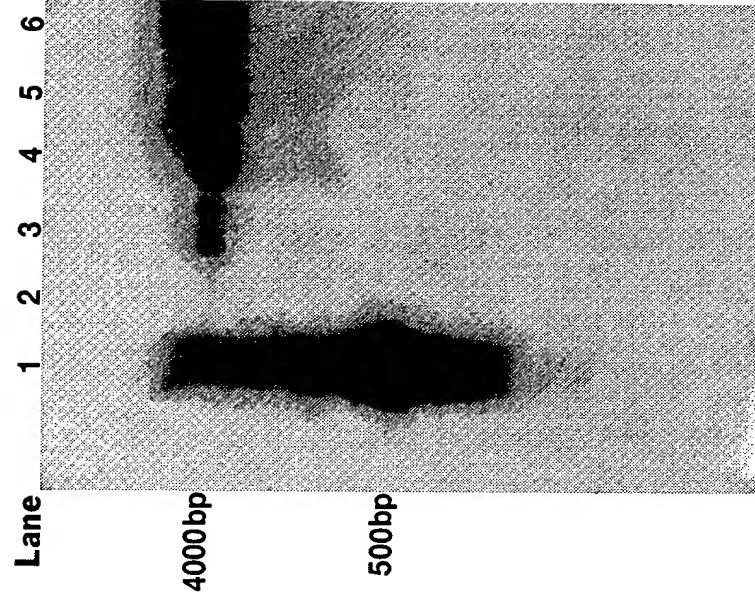


*Fig. 4.2*

**A.**

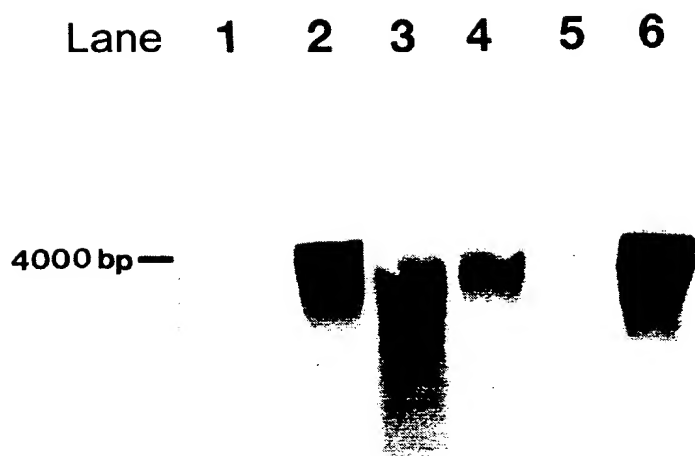


**B.**



*Fig. 4.3*

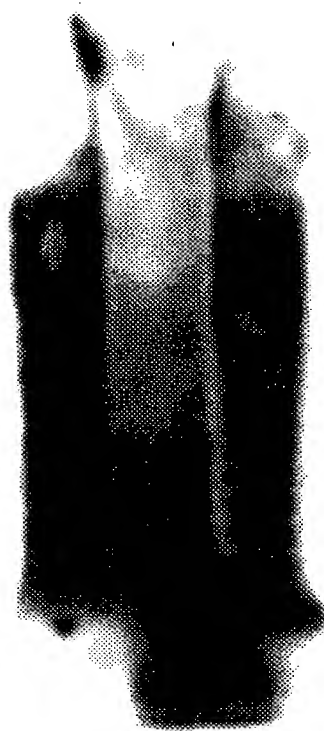
2023-09-20 09:29:29



*Fig. 4.4*

Lane	1	2	3	4	5
------	---	---	---	---	---

2027 2027 2027 2027 2027



23130

9416

4361

2322

2027

564

*Fig. 4.5.*

T<sub>m</sub> 13.17 cDNA

1 AGTGGATCCAAAGAATTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT  
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA  
L I L L V T V Q A L T E A Q I E K L N K  
↑ Forward Primer

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAGCTC  
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTCGTGGCCAGGA  
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA  
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAATCATCAATAAGTGCGCCGTCAAGA  
K V T D N D E E T E K I I N K C A V K R  
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA  
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC  
F S P V D \*

481 ATATAAAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG  
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGCCCATCGTTTTCCACCC

Fig. 4.6a

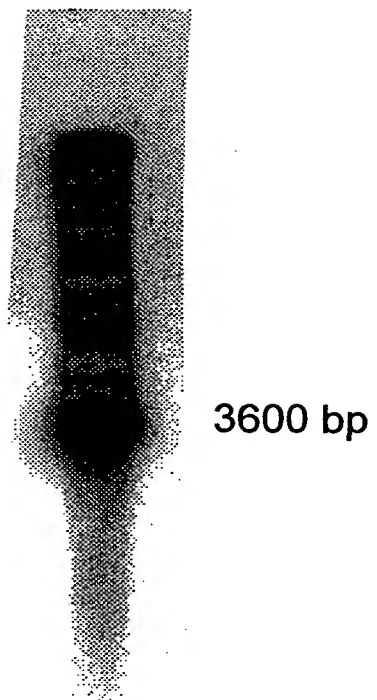
		Forward Primer									
2-2		L T D E Q I Q K R N K I S K E C Q Q V S	G V S Q E T	I D K V R T G V L V							
Tm 13.17		L T E A Q I E K L N K I S K K C Q N E S	G V S Q E I	I T K A R N G D W E							
B2		L T E E D L Q L L R Q T S A E C K T E S	G A S E A V I K K A R K G D L E								
AFP-3		E T P R E K L K Q H S D A C K A E S	G V S E E S	L N K V R N R E E V							
2-2		D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H									
Tm 13.17		D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K									
B2		D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R									
AFP-3		D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E									
		Reverse Primer									
2-2		V A S D E E V D K I V Q K C V V K K	A T P E E T	A Y D T F K C I Y D S							
Tm 13.17		V T D N D E E T E K I I N K C A V K R	D T V E E T	V F N T F K C V M K N							
B2		V T N D D E E S E K I V E K C T V T E	D T P E D T	A F E V T K C V L K D							
AFP-3		N S E H P E K V D D L V A K C A V K K	D T P Q H S	S A D F F K C V H D N							
2-2		K P D F S P I D									
Tm 13.17		K P K F S P V D									
B2		K P N F F G D L F V									
AFP-3		R S									

Fig. 4.6b

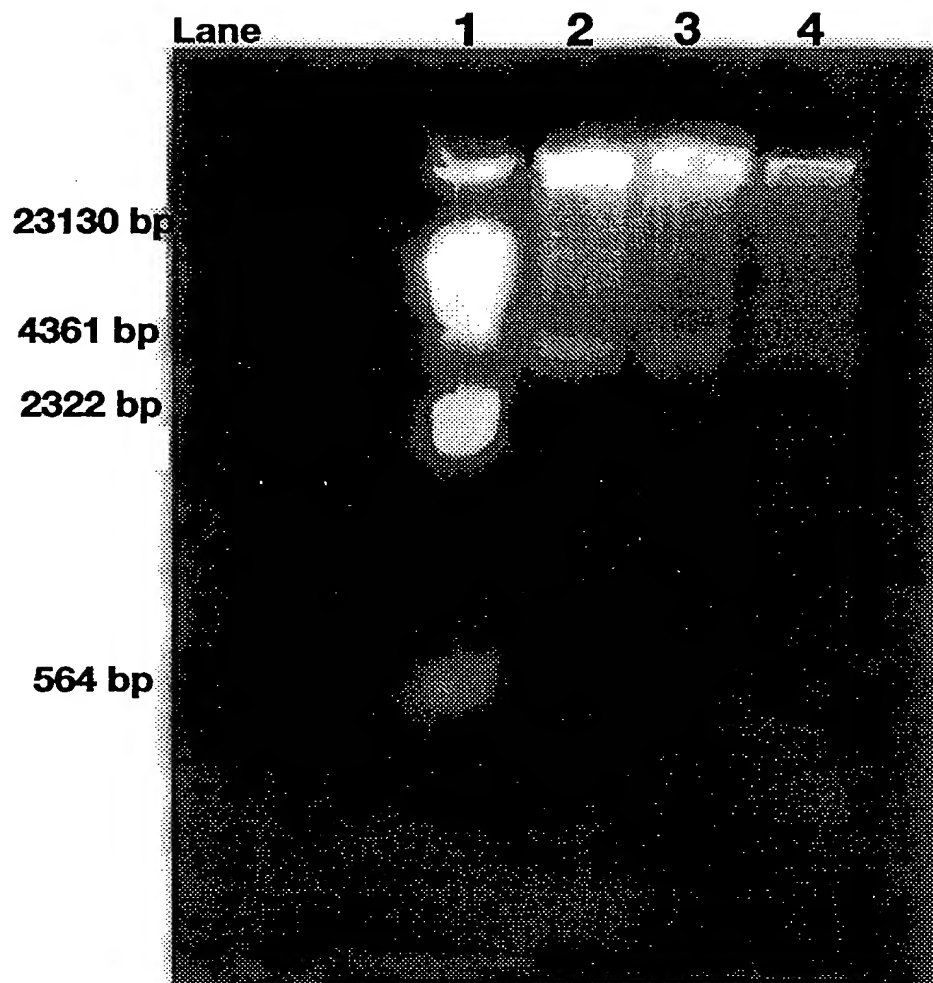
Primer	percent % composition				Melting Temperature (°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

Fig. 4.6c

202720 964960



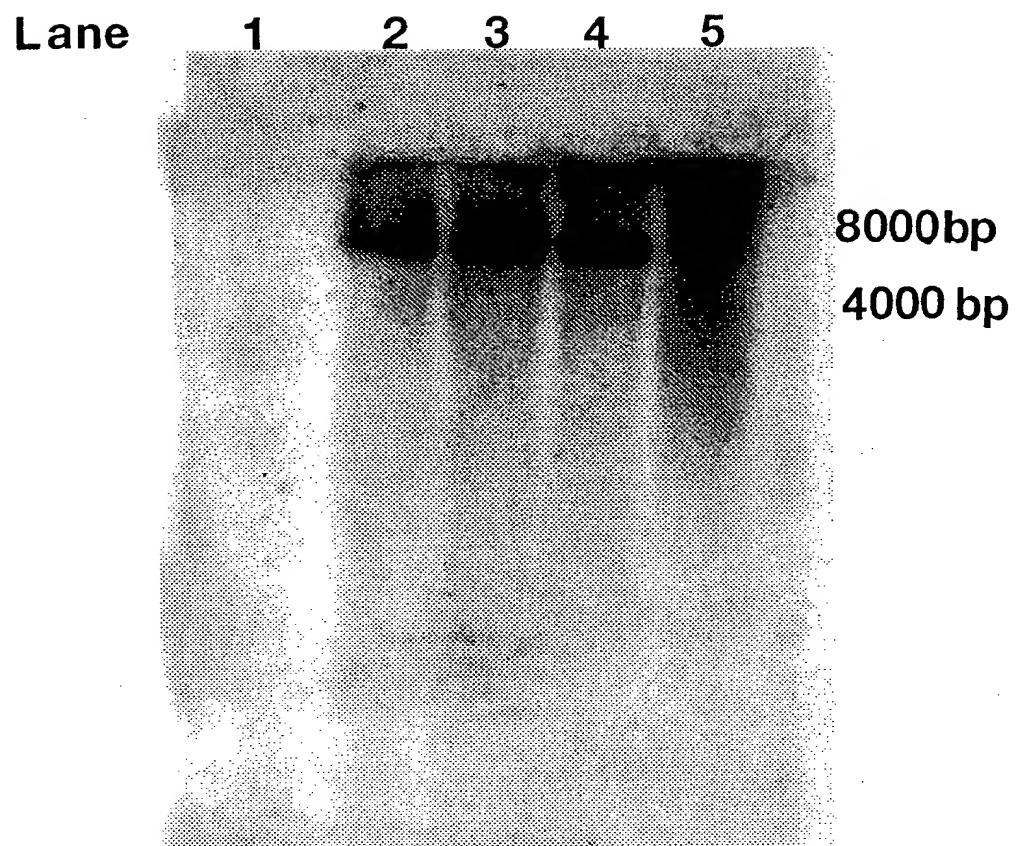
*Fig. 4.7*

[illegible]

*Fig. 4.8*



090799.0300



*Fig. 4.9*

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC  
                   M K L L L C F A F A A  
 47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA  
    I V I G A Q A L T D E Q I Q K  
 92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC  
    R N K I S K E C Q Q V S G V S  
 137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT  
    Q E T I D K V R T G V L V D D  
 182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA  
    P K M K K H V L C F S K K T G  
 226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTA CTCAAAGCC  
    V A T E A G D T N V E V L K A  
 271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG  
    K L K H V A S D E E V D K I V  
 316 CAGAAAGTGC GTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT  
    Q K C V V K K A T P E E T A Y  
 361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT  
    D T F K V I Y D S K P D F S P  
 406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT  
    I D  
 451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

*Fig. 4.10a*

Predicted Amino Acid

Composition of 3-4

Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

*Fig. 4.10b*

1    GGCACGAGCAAAAATGGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC  
           M    K    L    L    L    C    F    A    F    A    A

47    ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA  
           I    V    I    G    A    Q    A    L    T    D    E    Q    I    Q    K

92    AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC  
           R    N    K    I    S    K    E    C    Q    Q    E    S    G    V    S

137    CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT  
           Q    E    T    I    D    K    V    R    T    G    V    L    V    D    D

182    CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAACTGGA  
           P    K    M    K    K    H    V    L    C    F    S    K    R    T    G

226    GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
           V    A    T    E    A    G    D    T    N    V    E    V    L    K    A

271    AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG  
           K    L    K    H    V    A    S    D    E    E    V    D    K    I    V

316    CAGAAGTGC GTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT  
           Q    K    C    V    V    K    K    A    T    P    E    E    T    A    Y

361    GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT  
           D    T    F    K    V    I    Y    D    S    K    P    D    F    S    P

406    ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAAATAAAGGT  
           I    D    \*

451    ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

*Fig. 4.11a*

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.11b

1    GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC  
                           M    K    L    L    L    C    F    A    F    A    A

47    ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA  
       I    V    I    G    A    Q    A    L    T    D    E    Q    I    Q    K

92    AGGAACAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC  
       R    N    K    I    S    K    E    C    Q    Q    E    S    G    V    S

137    CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT  
       Q    E    T    I    D    K    V    R    T    G    V    L    V    D    D

182    CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA  
       P    K    M    K    K    H    V    L    C    F    S    K    R    T    G

226    GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
       V    A    T    E    A    G    D    T    N    V    E    V    L    K    A

271    AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG  
       K    L    K    H    V    A    S    D    E    E    V    D    K    I    V

316    CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT  
       Q    K    C    V    V    K    K    A    T    P    E    E    T    A    Y

361    GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT  
       D    T    F    K    V    I    Y    D    S    K    P    D    F    S    P

406    ATTGATTAAATTGTTTTGTATTTGGCTGAATTTTGACAATAAAGGT  
       I    D    .

polyadenylation signal

451    ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

poly (A) tail

*Fig. 4.12a*

# Predicted Amino Acid

## Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

### Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.12b

[illegible]



2-2  
2-3  
3-4  
3-9  
7-5

↓

MKLLLCFAFAAIVIGAAALTDEQIQKRNKISKKECQQVSGVSSQETIDKVGVLV  
 MKLLLCFAFAAIVIGAAALTDEQIQKRNKISKKECQQVSGVSSQETIDKVGVLV  
 MKLLLCFAFAAIVIGAAALTDEQIQKRNKISKKECQQVSGVSSQETIDKVGVLV  
 MKLLLCFAFAAIVIGAAALTDEQIQKRNKISKKECQQVSGVSSQETIDKVGVLV  
 MKLLLCFAFAAIVIGAAALTDEQIQKRNKISKKECQQVSGVSSQETIDKVGVLV

2-2  
2-3  
3-4  
3-9  
7-5

DDPKMKKHVLCFFSKKKTGVAATEAGDVTNVEVLKAKLKHVVASDEEEVDKIVQKCVVKK  
 DDPKMKKHVLCFFSKKKTGVAATEAGDVTNVEVLKAKLKHVVASDEEEVDKIVQKCVVKK  
 DDPKMKKHVLCFFSKKKTGVAATEAGDVTNVEVLKAKLKHVVASDEEEVDKIVQKCVVKK  
 DDPKMKKHVLCFFSKKKTGVAATEAGDVTNVEVLKAKLKHVVASDEEEVDKIVQKCVVKK  
 DDPKMKKHVLCFFSKKKTGVAATEAGDVTNVEVLKAKLKHVVASDEEEVDKIVQKCVVKK

2-2  
2-3  
3-4  
3-9  
7-5

ATPEEETAYDTFFKCIYDSKPPDFSPI D\*  
 ATPEEETAYDTFFKCIYDSKPPDFSPI D\*  
 ATPEEETAYDTFFKCIYDSKPPDFSPI D\*  
 ATPEEETAYDTFFKCIYDSKPPDFSPI D\*  
 ATPEEETAYDTFFKCIYDSKPPDFSPI D\*

Fig. 4.14

MW (kDa)	AA (#)	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	(% mole)										% most hydrophilic		
										Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser		Thr	
<b>Tm 12.86</b>	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3
<b>Tm 13.17</b>	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.41	0	0	7.12	15.6	3.31	6.14	32.14
<b>2-2</b>	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
<b>2-3</b>	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
<b>3-4</b>	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24
<b>3-9</b>	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38
<b>7-5</b>	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23

*Fig. 4.15*

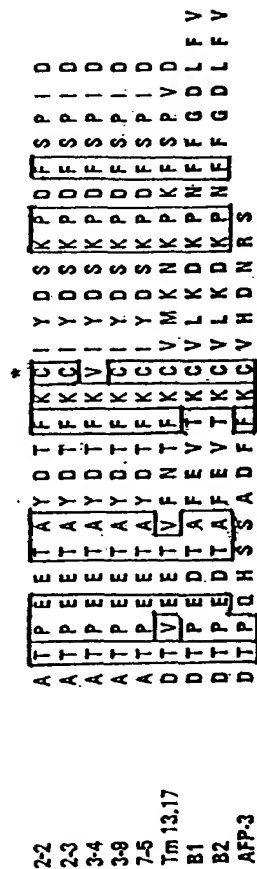
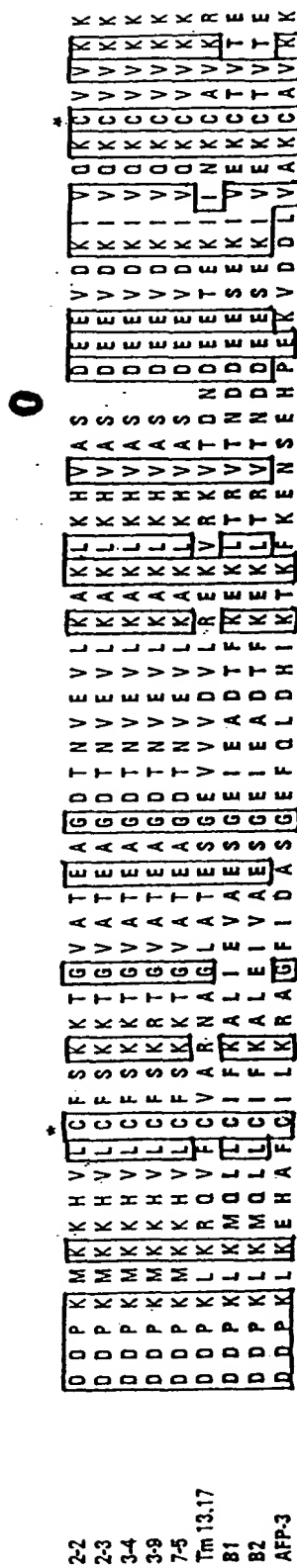
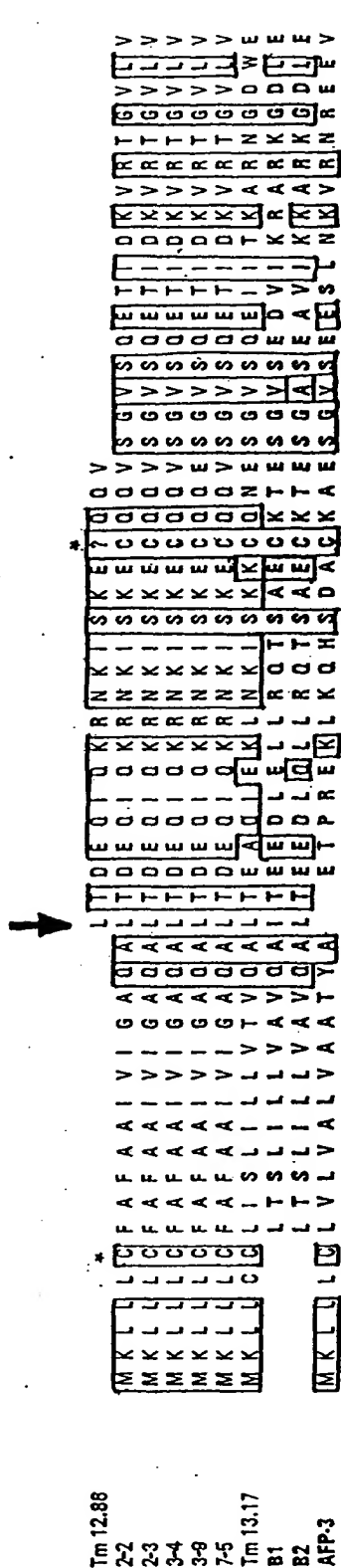


FIG 4.16

\* = conserved cysteine (yellow)

**Boxed** = conserved residues in  $\geq 7$  Genes (blue or orange)

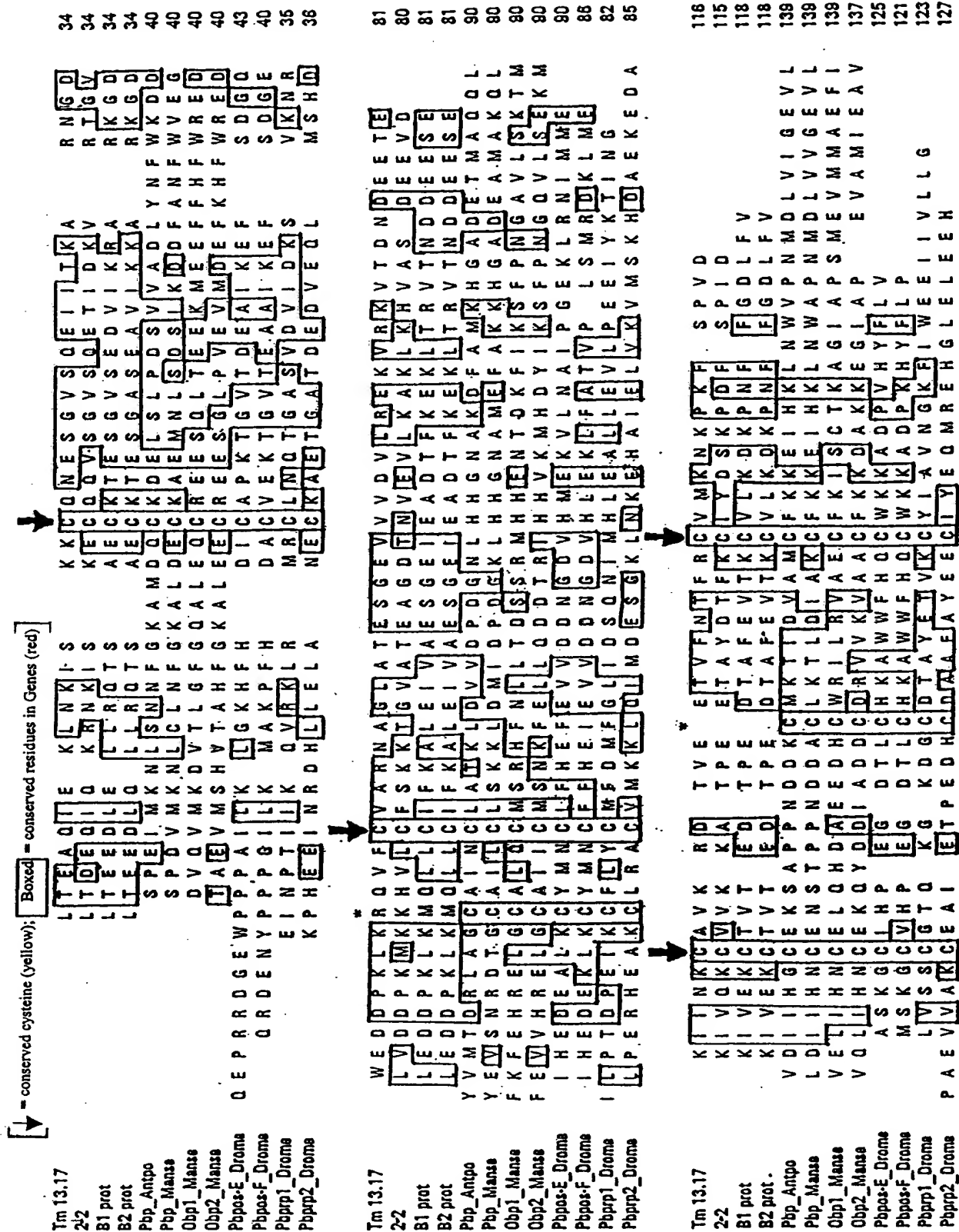


Fig. 4.17



## NUCLEOTIDE SEQUENCES

PERCENT SIMILARITY

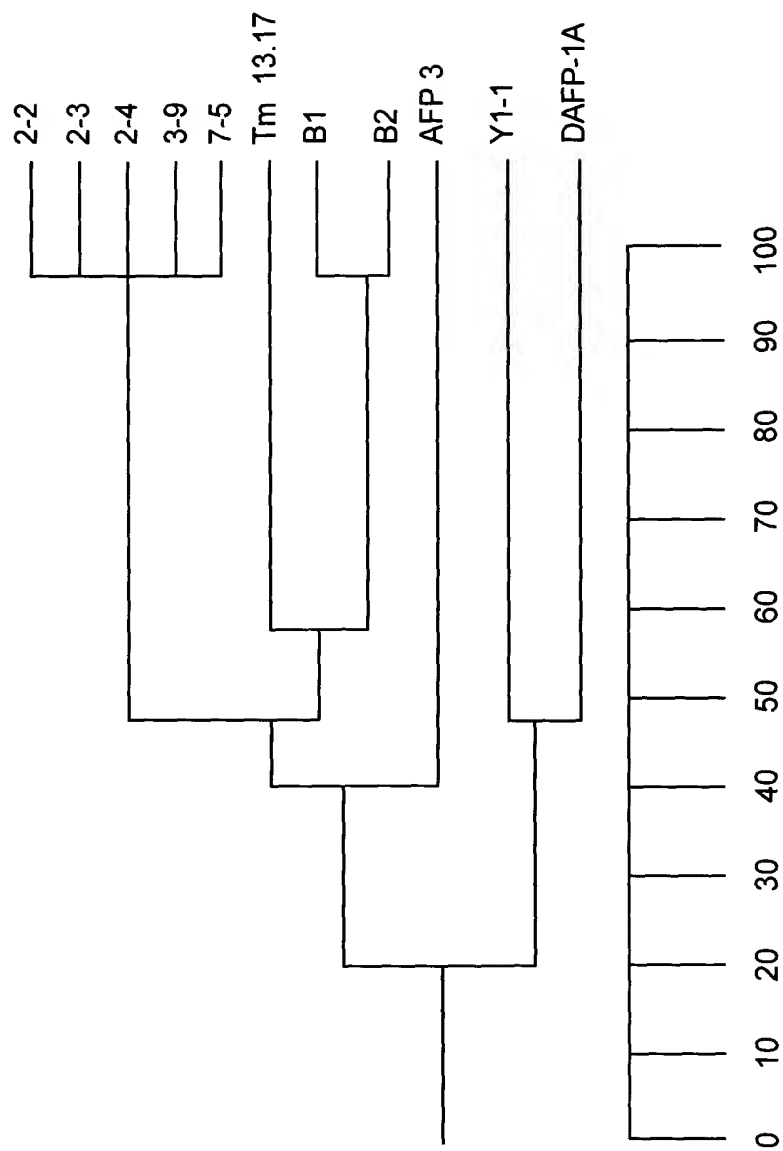
	1 <sup>2-2</sup>	2 <sup>2-3</sup>	3 <sup>3-4</sup>	4 <sup>3-9</sup>	5 <sup>7-5</sup>	6 <sup>Tm13.17</sup>	7 <sup>B1</sup>	8 <sup>AFP-3</sup>	9 <sup>YL-1</sup>	10 <sup>DAFP-1A</sup>		
PERCENT DIVERGENCE	1	2	3	4	5	6	7	8	9	10	1	2-2
1		99.1	97.3	98.4	98.2	50.4	42	42.4	20.7	20.9	1	2-2
2	0.9		99	99	99	51.5	43.2	42.7	20.2	21.3	2	2-3
3	1.6	60		98	98	50.3	42	42.1	20	20	3	3-4
4	1.6	20	80		98.4	51.3	43.7	43.6	20.4	22	4	3-9
5	1.8	25	75	45		50.4	42.5	42.9	22.2	23.1	5	7-5
6	36.9	36.4	37.2	36.4	37.1		57.2	37.4	23.3	21	6	Tm 13.17
7	39.9	41.2	41.7	40.7	41.2	30.2		39.3	21.9	22.1	7	B1
8	41.8	42.4	43.1	42.3	42.3	45.3	49.4		21.8	23.1	8	AFP-3
9	48.7	58.6	52	51.2	51.9	61.7	62.2	58.2		45.6	9	YL-1
10	51.4	62.7	46.4	46.5	46.5	60	58.1	61.8	35.5		10	DAFP-1A
	1	2	3	4	5	6	7	8	9	10		

## AMINO ACID SEQUENCES

PERCENT SIMILARITY

	1 <sup>2-2</sup>	2 <sup>2-3</sup>	3 <sup>3-4</sup>	4 <sup>3-9</sup>	5 <sup>7-5</sup>	6 <sup>Tm13.17</sup>	7 <sup>B1</sup>	8 <sup>AFP-3</sup>	9 <sup>YL-1</sup>	10 <sup>DAFP-1A</sup>		
PERCENT DIVERGENCE	1	2	3	4	5	6	7	8	9	10	1	2-2
1		100	99.1	99.1	100	51.3	37.4	35.2	11.6	12	1	2-2
2	0		99.1	99.1	100	51.3	37.4	35.2	11.6	12	2	2-3
3	0.9	0.9		98.3	99.1	50.4	36.5	34.3	11.6	12	3	3-4
4	0.9	0.9	1.7		99.1	51.3	37.4	36.1	10.7	12	4	3-9
5	0	0	0.9	0.09		51.3	37.4	35.2	11.6	12	5	7-5
6	46.1	46.1	47	46.1	46.1		47.4	39.8	13.4	13.9	6	Tm 13.17
7	59.1	59.1	60	59.1	59.1	51.7		37	11.6	11.1	7	B1
8	61.7	61.7	62.6	60.7	61.7	60.2	63		10.2	8.3	8	AFP-3
9	86.7	86.7	85.7	85.7	85.7	86.8	84.2	87.5		55.6	9	YL-1
10	88.3	88.3	86.4	84.5	85.4	89.1	82.7	90.5	40.2		10	DAFP-1A
	1	2	3	4	5	6	7	8	9	10		

Fig. 4.19

[illegible]

*Fig. 4.20*

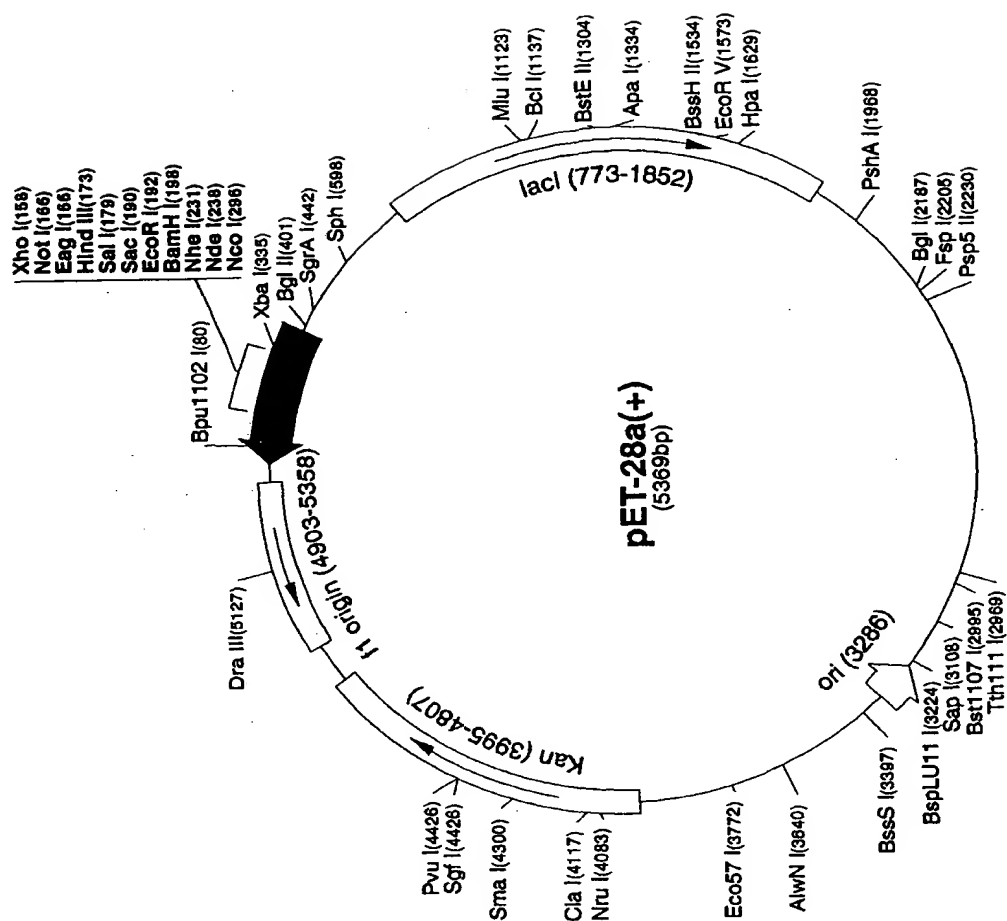


Fig. 5.0



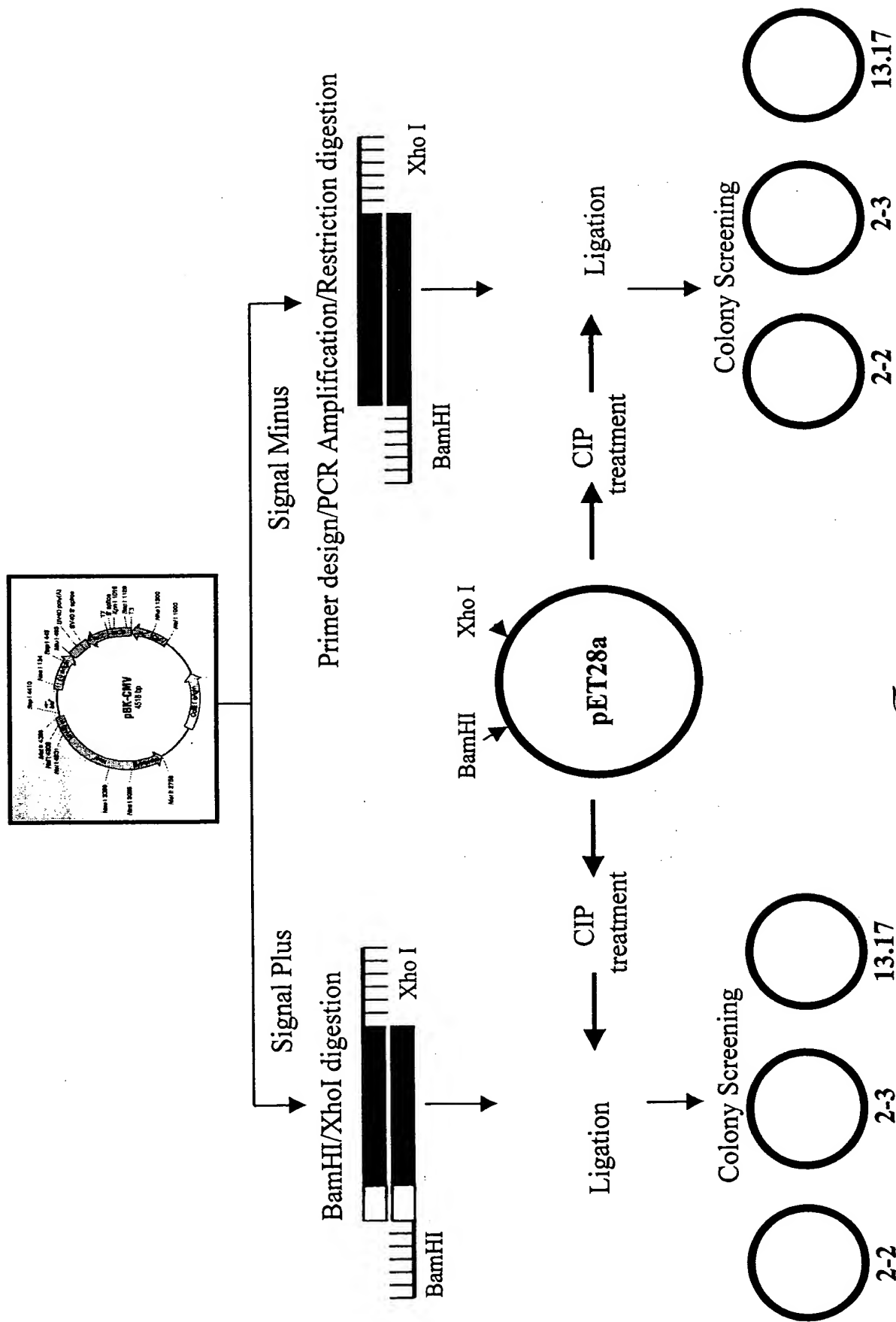


Fig. 5.1

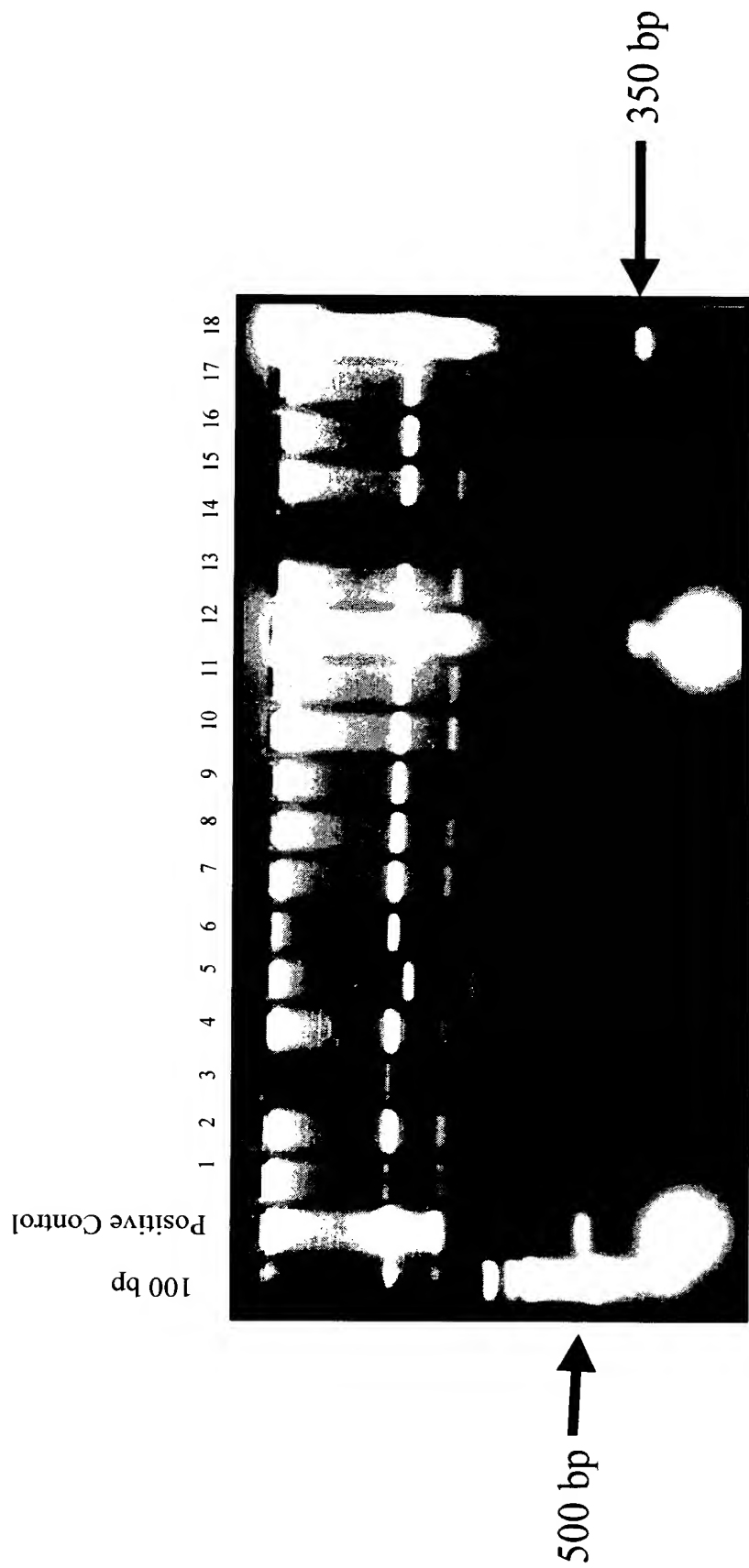


Fig. 5.2

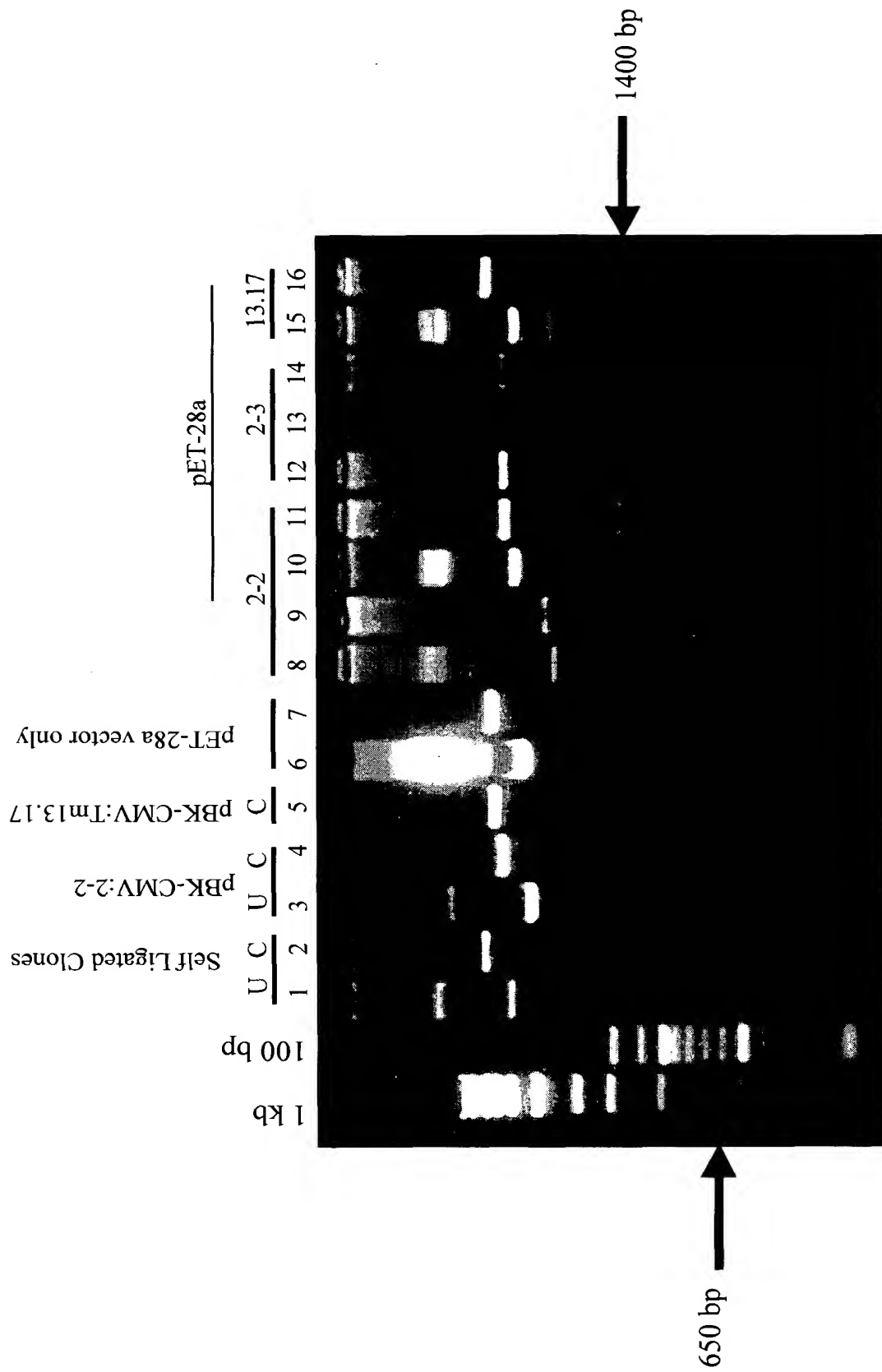


Fig. 5.3

202720-96294850

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTCGCCGCC  
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA  
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC  
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT  
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA  
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG  
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT  
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT  
D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT  
I D

451 ACTATCGTTATGTAAAAA

polyadenylation signal

poly (A) tail

Fig. 8.44

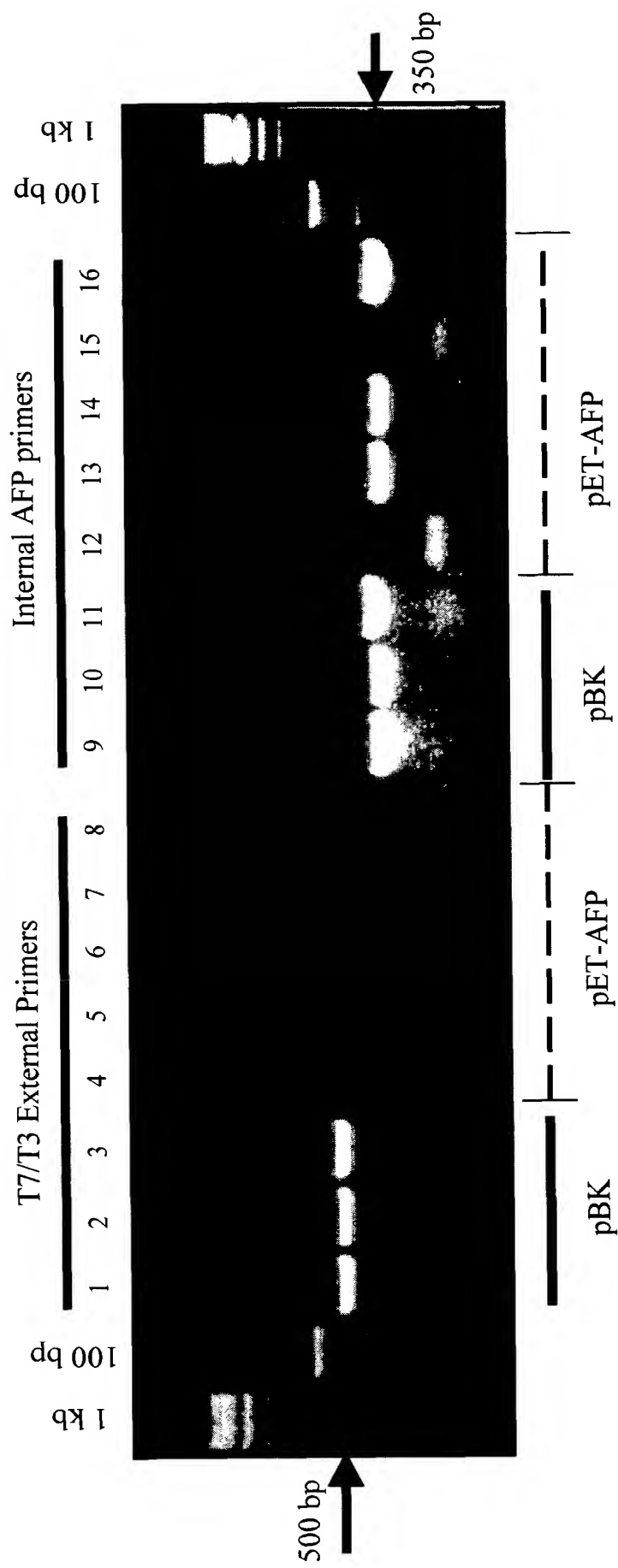
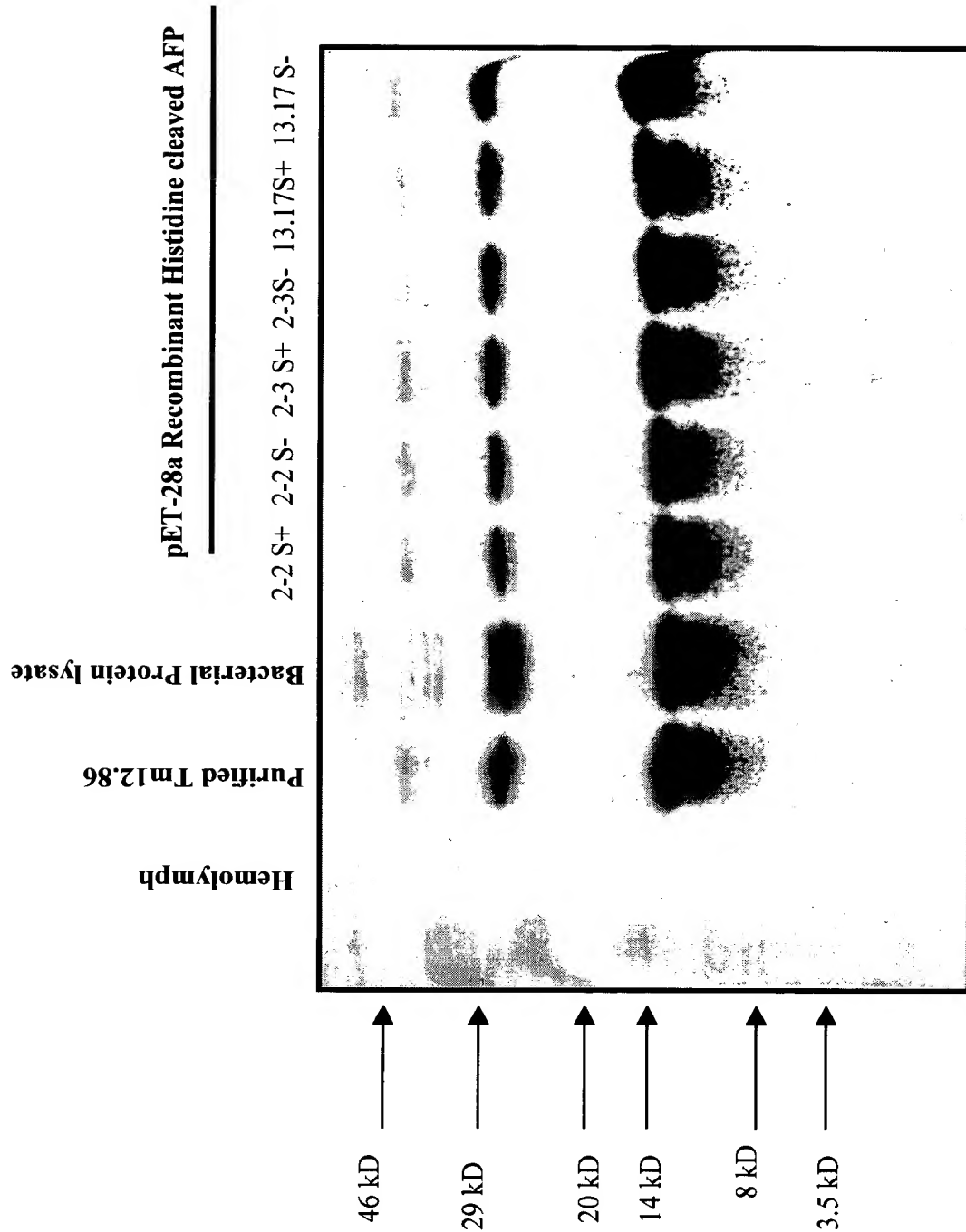


Fig. 5.4



Fig. 5.5



*Fig 5.6*

His-tagged Clone 2.2 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AFP Start Codon	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
N-terminal of mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

Fig. 5.7



# THE UNIVERSITY OF CHICAGO

*Fig. 5.8*

His-tagged clone 2.3 with signal sequence		
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG		50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC		96
Met Gly Ser Ser His His His His His His Ser		
-55 -50		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-45 -40 -35		
AFP Start Codon		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG		186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met		
-30 -25 -20		
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT		231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala		
-15 -10 -5		
N-terminal of Mature AFP		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC		276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser		
1 5 10		
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC		321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp		
15 20 25		
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG		366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys		
30 35 40		
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC		411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala		
45 50 55		
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG		456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val		
60 65 70		
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC		501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val		
75 80 85		
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT		546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys		
90 95 100		
Stop Codon		
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA		595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *		
105 110 115		
Polyadenylation signal Poly-A tail		
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA		645
AAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT		682

Fig. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
<div>His-tag Start Codon</div> <div>AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC</div> <div>Met Gly Ser Ser His His His His His His Ser</div> <div>-30 -25</div>	96
<div>AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT</div> <div>Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly</div> <div>-20 -15 -10</div>	141
<div>N-terminal of mature AFP</div> <div>GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG</div> <div>Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln</div> <div>-5 1 5</div>	186
<div>AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG</div> <div>Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val</div> <div>10 15 20</div>	231
<div>TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT</div> <div>Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp</div> <div>25 30 35</div>	276
<div>GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT</div> <div>Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr</div> <div>40 45 50</div>	321
<div>GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA</div> <div>Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys</div> <div>55 60 65</div>	366
<div>GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC</div> <div>Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile</div> <div>70 75 80</div>	411
<div>GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT</div> <div>Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala</div> <div>85 90 95</div>	456
<div>TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT</div> <div>Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser</div> <div>100 105 110</div>	501
<div>Stop Codon</div> <div>CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT</div> <div>Pro Ile Asp *</div> <div>115</div>	543

*Fig. 5.10*

His-tagged Tm 13.17 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

His-tag Start Codon  
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His Ser  
-65 -60 -55

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-50 -45 -40

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile  
-35 -30 -25

AFP Start Codon  
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC 231  
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser  
-20 -15 -10

N-terminal of mature AFP  
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT 276  
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile  
-5 1 5

GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA 321  
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly  
10 15 20

GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG 366  
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu  
25 30 35

GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC 411  
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn  
40 45 50

GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG 456  
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu  
55 60 65

AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG 501  
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu  
70 75 80

AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG 546  
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu  
85 90 95

ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG 595  
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys  
100 105 110

Stop Codon  
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG 643  
Phe Ser Pro Val Asp \*  
115

Polyadenylation signal Poly-A tail  
TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA 693

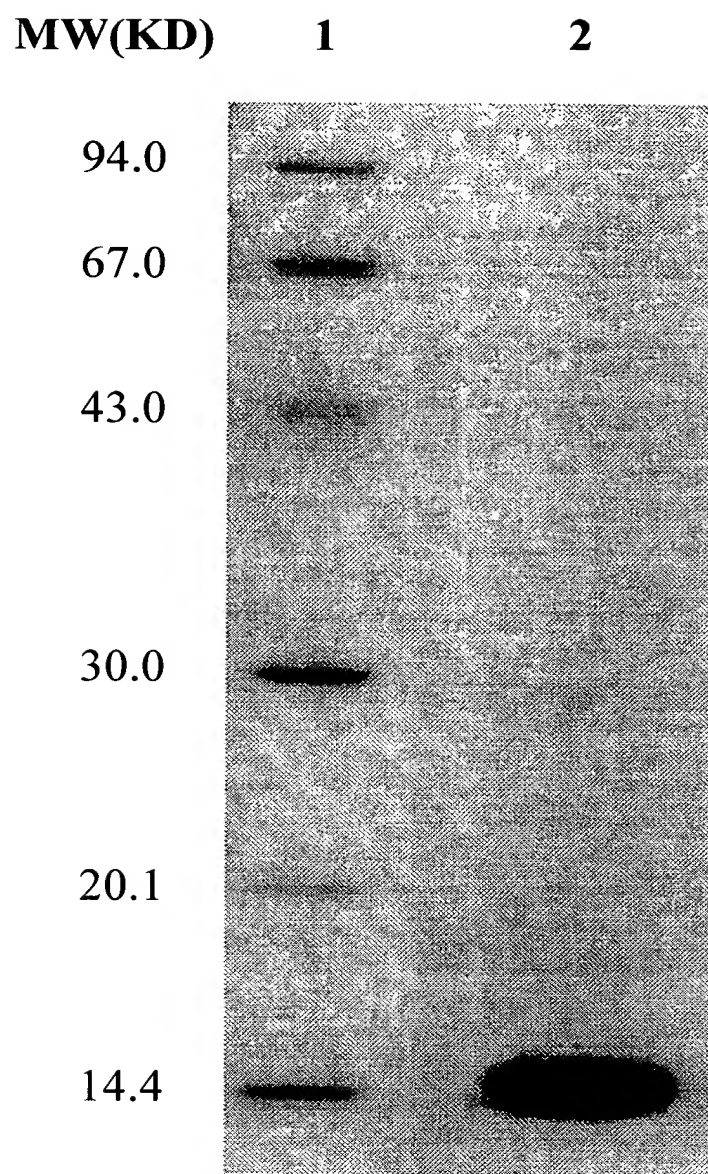
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TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT 777

Fig. 5.11

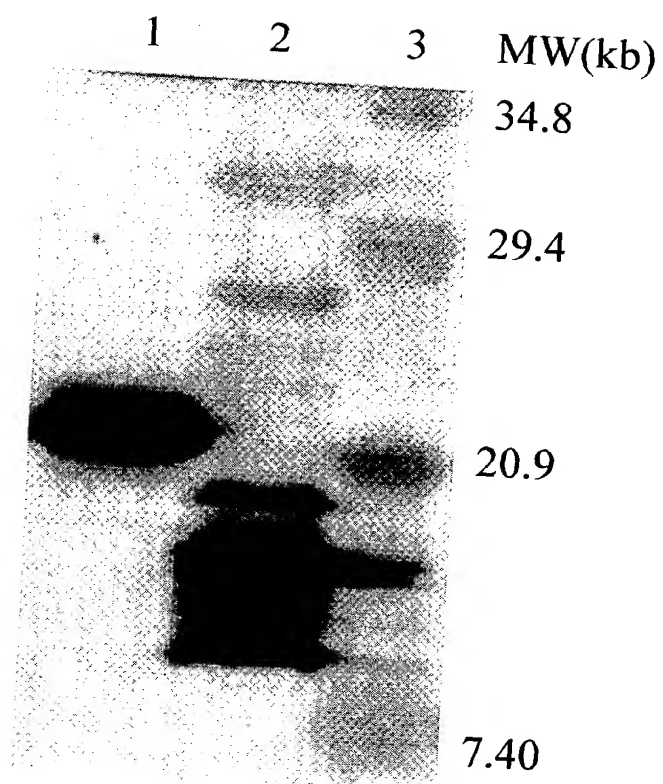
His-tagged Tm 13.17 without signal sequence	
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
Stop Codon	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

Fig. 5.12



*Fig. 6.0*

20230362060



*Fig. 6.1*



*Fig. 6.2*



Tm 13.17 S-graph data

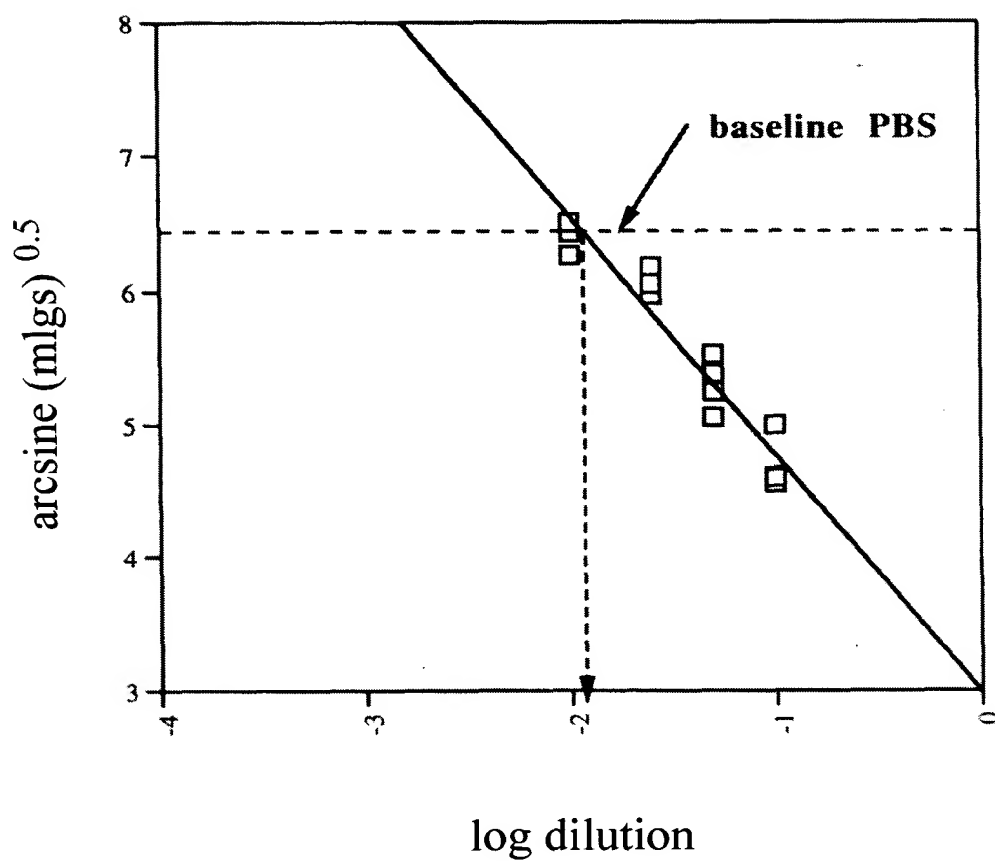


Fig. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Fig. 7.1

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of Tm12.84	Tm13.17	Consensus with Tm13.17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		A	C	N
2	G	G	C	C	G	C	G	N		N	A	N
3	A	A	A	A	A	G	A	R		N	G	R
4	G	G	A	G	G	A	C	N		N	A	N
5	C	C	C	C	C	C	T	N		N	T	N
6	A	A	A	A	A	A	A	N		N	C	N
7	A	A	A	A	A	A	C	N		N	G	N
8	A	A	A	A	A	A	A	N		N	A	N
9	A	A	A	A	A	A	A	A		N	A	A
10	A	A	A	A	A	A	G	R		A	G	R
11	A	A	A	A	A	A	.	.		.	.	.
12	A	A	A	A	A	A	.	.	A?	A	A	A
13	T	T	T	T	T	T	T	T	T?	T	T	T
14	G	G	G	G	G	G	G	G	G?	G	G	G
15	A	A	A	A	A	A	A	A		A	A	A
16	A	A	A	A	A	A	A	A		A	A	A
17	A	A	A	A	A	A	G	R		A	R	R
18	C	C	C	C	C	C	T	Y		T	C	T
19	C	C	C	C	C	C	T	T		T	T	T
20	C	C	C	C	C	C	T	T		T	T	T
21	C	C	C	C	C	C	T	C/G		C/G	C	C/G
22	C	C	C	C	C	C	T	C		C	C	C
23	T	T	T	T	T	T	T	T		T	T	T
24	T	T	T	T	T	T	T	T		T	T	T
25	T	T	T	T	T	T	T	T		T	T	T
26	T	T	T	T	T	T	T	T		T	T	T
27	G	G	G	G	G	G	T	N		N	T	N
28	T	T	T	T	T	T	T	T		T	T	T
29	G	G	G	G	G	G	T	G		G	T	G
30	T	T	T	T	T	T	C	Y		Y	T	Y
31	T	T	T	T	T	T	T	T		T	T	T
32	T	T	T	T	T	T	T	T		T	T	T
33	T	T	T	T	T	T	T	T		T	T	T
34	G	G	G	G	G	G	A	T/A		T/A	T	T/A
35	C	C	C	C	C	C	A	R		R	G	R
36	G	G	G	G	G	G	T	N		N	T	N
37	T	T	T	T	T	T	T	T		T	C	T
38	T	T	T	T	T	T	T	T		T	C	T
39	C	C	C	C	C	C	C	C		C	T	T
40	G	G	G	G	G	G	C	G/C		G/C	G	G/C
41	C	C	C	C	C	C	C	Y		Y	T	Y
42	C	C	C	C	C	C	C	C		C	T	C
43	C	C	C	C	C	C	C	C		C	T	C
44	C	C	C	C	C	C	C	C		C	T	C
45	C	C	C	C	C	C	C	C		C	T	C
46	A	A	A	A	A	A	T	N		N	T	N
47	T	T	T	T	T	T	C	G		G	T	G
48	C	C	C	C	C	C	T	T		T	T	T
49	T	T	T	T	T	T	T	T		T	T	T
50	T	T	T	T	T	T	T	T		T	T	T
51	C	C	C	C	C	C	A	C/G		C/G	C	C/G
52	A	A	A	A	A	A	T	R		R	T	R
53	T	T	T	T	T	T	C	T		T	C	T
54	C	C	C	C	C	C	C	R		R	C	R
55	G	G	G	G	G	G	C	G/C		G/C	A	G/C
56	A	A	A	A	A	A	A	A		A	C	A
57	G	G	G	G	G	G	A	G		A	G	A
58	C	C	C	C	C	C	T	Y		Y	C	Y
59	T	T	T	T	T	T	C	A		A	T	A
60	C	C	C	C	C	C	A	A		A	G	A
61	A	A	A	A	A	A	G	G		G	C	G
62	G	G	G	G	G	G	C	C		C	C	C
63	G	G	G	G	G	G	C	C		C	C	C
64	G	G	G	G	G	G	C	C		C	C	C
65	C	C	C	C	C	C	T	T		T	T	T
66	T	T	T	T	T	T	C	C		C	T	C
67	C	C	C	C	C	C	T	T		T	T	T
68	T	T	T	T	T	T	C	C/G		C/G	A	C/G
69	C	C	C	C	C	C	A	C		C	A	C
70	A	A	A	A	A	A	C	C		C	T	C
71	C	C	C	C	C	C	C	C		C	T	C
72	G	G	G	G	G	G	A	G		G	A	G
73	A	A	A	A	A	A	Y	A		A	A	A
74	C	C	C	C	C	C	G	G		G	A	G
75	A	A	A	A	A	A	A	A		A	A	A
76	A	A	A	A	A	A	A	A		A	A	A
77	A	A	A	A	A	A	A	A		A	A	A
78	C	C	C	C	C	C	C	C		C	A	C
79	A	A	A	A	A	A	A	A		A	C	A
80	G	G	G	G	G	G	A	A		A	C	A
81	A	A	A	A	A	A	T	T		T	C	T
82	T	T	T	T	T	T	A	A		A	T	A
83	A	A	A	A	A	A	C	C		C	T	C
84	C	C	C	C	C	C	A	A		A	G	A
85	A	A	A	A	A	A	G	G		G	A	G
86	G	G	G	G	G	G	A	A		A	A	A
87	A	A	A	A	A	A	A	A		A	A	A
88	A	A	A	A	A	A	A	A		A	A	A
89	A	A	A	A	A	A	A	A		A	A	A
90	A	A	A	A	A	A	A	A		A	A	A
91	A	A	A	A	A	A	A	A		A	A	A
92	G	G	G	G	G	G	T	T		T	G	T
93	A	A	A	A	A	A	A	A		A	A	A
94	A	A	A	A	A	A	A	A		A	A	A
95	C	C	C	C	C	C	A	A		A	A	A
96	A	A	A	A	A	A	A	A		A	A	A
97	A	A	A	A	A	A	A	A		A	A	A
98	A	A	A	A	A	A	A	A		A	A	A
99	G	G	G	G	G	G	A	A		A	A	A
100	A	A	A	A	A	A	T	T		T	C	T
101	T	T	T	T	T	T	C	C		C	A	C
102	A	A	A	A	A	A	G	G		G	A	G
103	G	G	G	G	G	G	C	C		C	G	C
104	C	C	C	C	C	C	A	A		A	C	C
105	A	A	A	A	A	A	A	A		A	G	A
106	A	A	A	A	A	A	A	A		A	R	A
107	A	A	A	A	A	A	A	A		A	T	A
108	G	G	G	G	G	G	A	A		A	G	A
109	A	A	A	A	A	A	A	A		A	C	A
110	A	A	A	A	A	A	R	R		R	C	R
111	T	T	T	T	T	T	T	T		T	T	T
112	G	G	G	G	G	G	G	G		G	T	G
113	C	C	C	C	C	C	C	C		C	C	C
114	C	C	C	C	C	C	C	C		C	A	A
115	C	C	C	C	C	C	C	C		C	A	A
116	A	A	A	A	A	A	A	A		A	A	A
117	G	G	G	G	G	G	A	R		R	G	R

Fig. 7.2

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	A	N	A	N	G	N
119	A	A	A	A	A	A	T	A	C	N	C	N
120	G	G	G	G	G	G	G	N	T	O	T	N
121	T	T	T	T	T	T	A	T/A	C	A	A	G
122	G	G	G	G	G	G	A	R	A	R	T	A/T
123	T	T	T	T	T	T	A	T/A	A	T/A	C	R
124	C	C	C	C	C	C	G	C/G	G	C/G	T	T/A
125	C	C	C	C	C	C	T	G	T	G	C	C/G
126	G	G	G	G	G	G	G	G	G	G	G	G
127	A	A	A	A	A	A	A	G	A	A	A	A
128	G	G	G	G	G	G	G	G	G	G	G	G
129	A	A	A	A	A	A	T	T	T	T	T	T
130	G	G	G	G	G	G	G	G	G	G	G	G
131	T	T	T	T	T	T	T	T	T	T	T	T
132	C	C	C	C	C	C	C	C	C	C	C	C
133	C	C	C	C	C	C	C	C/G	C	C/G	T	C
134	C	C	C	C	C	C	C	C	C	C	T	G
135	C	C	C	C	C	C	C	C	C	C	A	A
136	C	C	C	C	C	C	C	C	C	C	A	A
137	A	A	A	A	A	A	A	A	A	A	A	A
138	A	A	A	A	A	A	A	A	A	A	A	A
139	G	G	G	G	G	G	A	G	A	G	A	A
140	A	A	A	A	A	A	A	A	A	A	A	A
141	G	G	G	G	G	G	A	G	A	G	A	A
142	A	A	A	A	A	A	A	A	A	A	A	A
143	C	C	C	C	C	C	T	C	T	R	T	N
144	A	A	A	A	A	A	A	G/C	Y	G/C	C	G/C
145	A	A	A	A	A	A	T	A	A	A	C	N
146	T	T	T	T	T	T	C	N	N	N	T	N
147	C	C	C	C	C	C	A	R	A	A	A	A
148	G	G	G	G	G	G	A	N	A	N	C	N
149	A	A	A	A	A	A	C	C	A	C	A	C
150	C	C	C	C	C	C	C	C	A	C	A	A
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	G	G	G	G	G	G	C	G	C	G	G	G
155	T	T	T	T	T	T	T	Y	Y	Y	T	Y
156	C	C	C	C	C	C	C	C	C	C	C	C
157	C	C	C	C	C	C	C	C	C	C	C	C
158	G	G	G	G	G	G	C	C	C	C	C	C
159	C	C	C	C	C	C	C	C	C	C	C	C
160	A	A	A	A	A	A	A	A	A	A	A	A
161	C	C	C	C	C	C	C	N	A	N	A	N
162	A	A	A	A	A	A	C	N	A	N	C	N
163	G	G	G	G	G	G	G	G	G	G	G	G/C
164	T	T	T	T	T	T	T	T	T	T	T	T
165	G	G	G	G	G	G	G	T/A	G	T/A	G	T/A
166	T	T	T	T	T	T	C	C	A	C	A	A
167	C	C	C	C	C	C	T	N	T	T	T	N
168	T	T	T	T	T	T	G	G	G	G	A	R
169	T	T	T	T	T	T	G	G	G	G	T	N
170	G	G	G	G	G	G	G	G	G	G	A	R
171	G	G	G	G	G	G	G	G	G	G	A	R
172	T	T	T	T	T	T	T	T/A	T	T/A	T	T/A
173	C	C	C	C	C	C	C	C/G	C	C/G	G	C/G
174	T	T	T	T	T	T	C	A	A	A	A	A
175	G	G	G	G	G	G	A	Y	G	Y	A	Y
176	A	A	A	A	A	A	C	G	A	C	A	A
177	T	T	T	T	T	T	G	A	T	A	C	C
178	G	G	G	G	G	G	A	G	G	G	G	G
179	A	A	A	A	A	A	T	C	C	C	C	C
180	T	T	T	T	T	T	C	C	C	C	C	C
181	C	C	C	C	C	C	C	Y	A	A	A	A
182	C	C	C	C	C	C	A	A	A	A	A	A
183	C	C	C	C	C	C	A	A	A	A	A	A
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	T	T	T	T	T	T	T	T	T	T	T	T
188	G	G	G	G	G	G	G	T	G	T	G	G
189	A	A	A	A	A	A	A	A	A	A	A	A
190	A	A	A	A	A	A	A	A	A	A	A	A
191	A	A	A	A	A	A	A	A	A	A	A	A
192	G	G	G	G	G	G	A	R	A	R	A	R
193	A	A	A	A	A	A	C	N	N	N	A	N
194	A	A	A	A	A	A	G	R	T	T	A	N
195	C	C	C	C	C	C	C	G/C	G	G/C	C	G/C
196	A	A	A	A	A	A	C	A	C	A	C	C
197	C	C	C	C	C	C	A	A	A	A	A	A
198	C	C	C	C	C	C	G	N	C	N	T	N
199	T	T	T	T	T	T	T	G	C	C	G	G
200	C	C	C	C	C	C	T	Y	T	T	C	Y
201	C	C	C	C	C	C	T	Y	T	T	T	Y
202	T	T	T	T	T	T	T	Y	T	T	T	Y
203	C	C	C	C	C	C	T	T	T	T	T	T
204	T	T	T	T	T	T	G	T	T	T	T	T
205	G	G	G	G	G	G	C	N	C	N	C	C
206	T	T	T	T	T	T	T	T	T	T	T	T
207	C	C	C	C	C	C	T	C	A	C	A	A
208	T	T	T	T	T	T	T	C/G	T	N	T	N
209	C	C	C	C	C	C	C	N	T	N	T	N
210	T	T	T	T	T	T	G	C	T	T	T	T
211	C	C	C	C	C	C	C	C	T	T	T	T
212	G	G	G	G	G	G	A	G/C	A	G/C	A	G/C
213	A	A	A	A	A	A	A	A	A	A	A	A
214	A	A	A	A	A	A	A	A	A	A	A	A
215	A	A	A	A	A	A	A	A	A	A	A	A
216	G	G	G	G	G	G	A	R	R	R	A	R
217	A	A	A	A	A	A	A	A	A	A	A	A
218	A	A	A	A	A	A	A	A	A	A	A	A
219	A	A	A	A	A	A	A	A	A	A	A	A
220	A	A	A	A	A	A	A	A	A	A	A	A
221	C	C	C	C	C	C	C	C	C	C	C	C
222	T	T	T	T	T	T	G	Y	T	T	T	T
223	G	G	G	G	G	G	G	G	A	R	G	R
224	A	A	A	A	A	A	A	A/T	A	A/T	A	A/T
225	G	G	G	G	G	G	T	G/C	T	N	T	N
226	T	T	T	T	T	T	T	T	A	R	C	N
227	G	G	G	G	G	G	G	G	T	Y	A	R
228	C	C	C	C	C	C	C	N	C	N	C	N
229	A	A	A	A	A	A	A	C	G	R	A	R
230	A	A	A	A	A	A	A	C/G	G	C/G	C	C/G
231	C	C	C	C	C	C	C	G	G	G	G	G
232	C	C	C	C	C	C	C	G	G	G	G	G
233	C	C	C	C	C	C	C	G	G	G	G	G
234	C	C	C	C	C	C	C	G	G	G	G	G
235	G	G	G	G	G	G	G	G	G	G	G	G

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFF-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	A	A	A	A	A	A	A	A	C	N
238	C	G	C	C	C	C	T	C	T	N	C	C/G
239	C	C	C	C	C	C	G	G	G	C/G	T	N
240	G	G	G	G	G	G	G	G	G	G	G	G
241	A	A	A	A	A	A	A	A	A	A	G	A/T
242	G	A	A	A	A	A	A	A	A	A	G	G
243	A	A	A	A	A	A	A	A	A	A	G	A
244	A	A	A	A	A	A	A	A	A	A	A	A
245	A	A	A	A	A	A	A	A	A	A	A	A
246	C	C	C	C	C	C	A	C/G	A	N	A	N
247	A	A	A	A	A	A	G	R	A	R	A	N
248	C	C	C	C	C	C	T	Y	T	Y	T	Y
249	A	A	A	A	A	A	G	C/G	T	N	C	N
250	A	A	A	A	A	A	T	R	A	A	A	A
251	A	A	A	A	A	A	T	A/T	A	A/T	A	A
252	T	T	T	T	T	T	G	N	G	N	C	N
253	G	G	G	G	G	G	T	G	C	Y	C	G/C
254	T	T	T	T	T	T	C	G	C	G	G	Y
255	G	G	G	G	G	G	G	G	C	G	G	G
256	A	A	A	A	A	A	A	A	A	A	A	A
257	G	G	G	G	G	G	A	G	A	G	C	G
258	A	A	A	A	A	A	C	G/C	C	G	C	G
259	T	T	T	T	T	T	G	G	A	R	C	N
260	A	A	A	A	A	A	T	R	C	R	A	N
261	C	C	C	C	C	C	T	Y	G	Y	A	N
262	T	T	T	T	T	T	T	T	T	T	T	T
263	C	C	C	C	C	C	G	C/G	C	C/G	T	N
264	A	A	A	A	A	A	A	A	A	A	A	A
265	A	A	A	A	A	A	A	A	A	A	A	A
266	A	A	A	A	A	A	A	A	A	A	A	A
267	G	G	G	G	G	G	G	R	G	R	A	R
268	C	C	C	C	C	C	A	S	G	C	G	N
269	C	C	C	C	C	C	A	N	A	N	C	C
270	C	C	C	C	C	C	A	C/G	G	C/G	G	C/G
271	A	A	A	A	A	A	A	A	A	A	A	A
272	C	C	C	C	C	C	A	A	A	A	A	A
273	C	C	C	C	C	C	G	G	G	G	T	N
274	T	T	T	T	T	T	T	C/G	T	T	T	T
275	G	G	G	G	G	G	G	G	T	G	C	G/C
276	A	A	A	A	A	A	A	A	A	A	A	A
277	A	A	A	A	A	A	A	R	C	N	A	N
278	C	C	C	C	C	C	G	G	A	G	G	G
279	A	A	A	A	A	A	A	N	A	N	A	R
280	C	C	C	C	C	C	A	A	G	R	A	N
281	A	A	A	A	A	A	G	N	G	N	A	N
282	T	T	T	T	T	T	T	G	T	N	A	N
283	G	G	G	G	G	G	C	T	G	N	A	N
284	T	T	T	T	T	T	T	G/C	A	N	C	N
285	G	G	G	G	G	G	G	R	C	N	T	N
286	C	C	C	C	C	C	A	C	A	N	C	N
287	C	C	C	C	C	C	T	Y	A	N	T	N
288	A	A	A	A	A	A	G	R	A	R	G	R
289	G	G	G	G	G	G	A	R	C	N	A	N
290	C	C	C	C	C	C	C	C	G	C/G	A	C/G
291							A	A	A	A	T	R
292							A	C	T	A/T	A	A
293							A	G	A	C/G	T	N
294							A	A	G	R	T	N
295	G	G	G	G	G	G	C	G	A	A/T	C	C
296	A	A	A	A	A	A	A	A	A	C/G	G	G
297	C	C	C	C	C	C	A	A	A	R	A	A
298	A	A	A	A	A	A	A	A	A	R	A	R
299	A	A	A	A	A	A	A	A	A	R	A	R
300	A	A	A	A	A	A	A	A	A	R	A	R
301	A	A	A	A	A	A	A	A	A	R	A	R
302	A	A	A	A	A	A	A	A	A	R	A	R
303	G	G	G	G	G	G	A	R	A	R	A	R
304	T	T	T	T	T	T	C	Y	G	Y	T	Y
305	G	G	G	G	G	G	T	N	A	N	C	N
306	A	A	A	A	A	A	G	A	A	R	A	R
307	C	C	C	C	C	C	A	C/G	A	N	A	N
308	A	A	A	A	A	A	A	A	A	R	A	R
309	A	A	A	A	A	A	A	A	A	N	A	N
310	A	A	A	A	A	A	A	A	A	R	A	R
311	A	A	A	A	A	A	A	A	A	R	A	R
312	A	A	A	A	A	A	A	A	A	R	C	N
313	T	T	T	T	T	T	A	A	T	A/T	T	A/T
314	C	C	C	C	C	C	T	C	T	T	T	T
315	G	G	G	G	G	G	C	R	G	C/G	G	C/G
316	T	T	T	T	T	T	T	T	T	N	T	Y
317	G	G	G	G	G	G	T	G/C	G	G/C	T	N
318	C	C	C	C	C	C	A	N	A	N	G	N
319	A	A	A	A	A	A	A	N	A	R	C	N
320	G	G	G	G	G	G	T	A	A	N	C	N
321	A	A	A	A	A	A	A	A	A	N	A	N
322	A	A	A	A	A	A	A	A	A	R	A	R
323	A	A	A	A	A	A	G	A	G	N	A	N
324	T	T	T	T	T	T	T	T	C	N	T	N
325	G	G	G	G	G	G	G	G	G	G/C	G	G/C
326	C	C	C	C	C	C	C	C	A	N	T	N
327	G	G	G	G	G	G	C	Y	C	G	G	G
328	T	T	T	T	T	T	G	G/C	G	G/C	C	G/C
329	G	G	G	G	G	G	T	A	T	N	G	N
330	T	T	T	T	T	T	C	T	A	N	T	N
331	C	C	C	C	C	C	A	A	C	N	A	N
332	A	A	A	A	A	A	A	A	A	N	A	N
333	A	A	A	A	A	A	A	A	A	N	A	N
334	A	A	A	A	A	A	A	A	A	N	A	N
335	A	A	A	A	A	A	A	A	A	G	A	G
336	A	A	A	A	A	A	A	A	A	A	A	A
337	A	A	A	A	A	A	A	A	A	R	A	R
338	A	A	A	A	A	A	A	A	A	R	A	R
339	G	G	G	G	G	G	A	G	A	N	G	N
340	C	C	C	C	C	C	A	N	A	N	A	N
341	C	C	C	C	C	C	T	Y	C	N	A	N
342	A	A	A	A	A	A	A	A	A	N	C	N
343	C	C	C	C	C	C	C	T	C	Y	C	Y
344	A	A	A	A	A	A	T	A	C	N	T	N
345	C	C	C	C	C	C	G	C/G	G	C/G	C	C/G
346	C	C	C	C	C	C	T	Y	T	N	T	N
347	A	A	A	A	A	A	T	A	A	R	C	N
348	A	A	A	A	A	A	T	G	A	A	A	A
349	G	G	G	G	G	G	A	A	A	R	A	R
350	A	A	A	A	A	A	A	A	A	R	A	R
351	G	G	G	G	G	G	A	A	A	R	A	R
352	A	A	A	A	A	A	A	A	A	A	A	A
353									T	A/T		A/T

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	A	A	A	A	A	C	C	N	T	N
356	C	C	C	C	C	C	C	G	G	C/G	C	C/G
357	G	G	G	G	G	G	G	G	G	G/C	T	N
358	C	C	C	C	C	C	T	Y	A	N	C	N
359	T	T	T	T	T	T	T	N	T	N	A	N
360	T	T	T	T	T	T	T	T	T	T	G	N
361	A	A	A	A	A	A	T	A/T	G	A	C	N
362	A	A	A	A	A	A	C	Y	A	N	C	N
363	G	G	G	G	G	G	A	R	A	R	G	N
364	A	A	A	A	A	A	A	A	G	A	C	A
365	C	C	C	C	C	C	T	A	T	N	T	N
366	A	A	A	A	A	A	A	C	T	A	C	A
367	C	C	C	C	C	C	T	Y	T	A/T	T	A/T
368	C	C	C	C	C	C	T	C	A	Y	T	Y
369	T	T	T	T	T	T	T	T	C	T	C	Y
370	T	T	T	T	T	T	T	T	C	T	T	Y
371	T	T	T	T	T	T	T	T	A	T	T	N
372	C	C	C	C	C	C	A	A	A	A	A	A
373	A	A	A	A	A	A	A	A	A	N	A	A
374	O	O	O	O	O	O	N	R	T	N	A	N
375	T	T	T	T	T	T	T	N	G	N	T	N
376	G	G	G	G	G	G	T	T	T	N	G	N
377	T	T	T	T	T	T	T	R	A	N	C	N
378	A	A	A	A	A	A	T	A	T	N	T	N
379	T	T	T	T	T	T	C	Y	T	T/A	T	T/A
380	T	T	T	T	T	T	A	A/T	G	T/A	C	N
381	T	T	T	T	T	T	T	C/G	A	N	A	N
382	A	A	A	A	A	A	G	R	A	R	G	R
383	C	C	C	C	C	C	A	A	A	N	A	A
384	G	G	G	G	G	G	A	N	A	A	C	A
385	A	A	A	A	A	A	A	A	G	R	T	R
386	C	C	C	C	C	C	A	A	A	N	A	N
387	A	A	A	A	A	A	A	R	A	A	A	A
388	C	C	C	C	C	C	C	Y	A	N	A	N
389	G	G	G	G	G	G	A	A	A	R	A	A
390	C	C	C	C	C	C	A	A	A	N	C	N
391	A	A	A	A	A	A	A	A	G	A	G	A
392	A	A	A	A	A	A	G	A	C	R	T	R
393	C	C	C	C	C	C	C	C	C	C	Y	Y
394	C	C	C	C	C	C	A	T/A	A	T/A	C	C
395	T	T	T	T	T	T					G	N
396												
397												
398	G	G	G	G	G	G	A	R	A	R		
399	A	A	A	A	A	A	T	A	A/T	A/T		
400	T	T	T	T	T	T	T	N	N	N		
401	T	T	T	T	T	T	T	T	T	Y		
402	T	T	T	T	T	T	T	T	T	T		
403	C	C	C	C	C	C	C	C	T	Y		
404	T	T	T	T	T	T	T	T	T	T		
405	O	O	O	O	O	O	C	C	T	V		
406	C	C	C	C	C	C	A	C	G	N		
407	C	C	C	C	C	C	C	C	A	C		
408	T	T	T	T	T	T	A	T/A	G	N		
409	A	A	A	A	A	A	G	R	A	R		
410	T	T	T	T	T	T	T	T	T	Y		
411	G	G	G	G	G	G	A	A	A	T		
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413	T	T	T	T	T	T	G	A	T	T		
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415	T	T	T	T	T	T	T	T	T	T		
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420	T	T	T	T	T	T	A	T/A	C	N		
421	T	T	T	T	T	T	C	Y	T	Y		
422	G	G	G	G	G	G	A	G/C	G	G/C		
423	T	T	T	T	T	T	C	T/A	A	T/A		
424	T	T	T	T	T	T	A	Y	A	N		
425	T	T	T	T	T	T	C	T/A	G	N		
426	T	T	T	T	T	T	A	G/C	C	G		
427	G	G	G	G	G	G	G	N	T	N		
428	T	T	T	T	T	T	A	A	T	A/T		
429	A	A	A	A	A	A	T	Y	T	Y		
430	T	T	T	T	T	T	T	T/A	G	N		
431	T	T	T	T	T	T	A	G	T	G		
432	G	G	G	G	G	G	T	N	G	A		
433	A	A	A	A	A	A	G	N	N	A		
434	C	C	C	C	C	C	A	N	A	A		
435	T	T	T	T	T	T	G	R	C	T		
436	G	G	G	G	G	G	A	A	A	A		
437	A	A	A	A	A	A	T	G	A	A/T		
438	A	A	A	A	A	A	T	R	A	R		
439	T	T	T	T	T	T	G	N	N	T		
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441	T	T	T	T	T	T	T	T	T	T		
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444	A	A	A	A	A	A	A	A	A	A		
445	C	C	C	C	C	C	A	A	A	A		
446							T	G	T	G		
447							G	G	T	A		
448							T	T	G	A		
449							G	G	T	A		
450							T	T	T	A		
451							C	C	G	C		
452							T	T	T	T		
453							T	T	T	T		
454							T	T	T	T		
455							T	T	T	T		
456							T	T	T	T		
457							T	T	T	T		
458							T	T	T	T		
459							T	T	T	T		
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461							T	T	T	T		
462							T	T	T	T		
463							T	T	T	T		
464							T	T	T	T		
465							T	T	T	T		
466							T	T	T	T		
467							T	T	T	T		
468							T	T	T	T		
469							T	T	T	T		
470							T	T	T	T		
471							T	T	T	T		

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A		A	A	A
473	A	A	A	A	A	A	A	A		A	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	T	N
479	G	G	G	G	G	G	G	N		N	T	N
480	T	T	T	T	T	T	T	N		N	T	N
481	A	A	A	A	A	A	A	N		N	A	N
482	A	C	C	C	C	C	T	Y		Y	A	A
483	T	T	T	T	T	T	T	T		T	A	A/T
484	A	A	A	A	A	A	C	N		N	G	N
485	T	T	T	T	T	T	T	T		T	A	A/T
486	C	C	C	C	C	C	G	N		N	A	N
487	G	T	T	G	G	G	A	R		R	A	R
488	T	T	T	T	T	T	T	T		T	A	T/A
489	T	T	T	T	T	T	G	N		N	A	N
490	A	A	A	A	A	A	T	N		N	A	N
491	T	T	T	T	T	T	A	N		N	A	R
492	G	G	G	G	G	G	A	N		R	A	N
493	A	A	A	A	A	A	A	A		A	A	N
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
497	A	A	A	A	A	A	A	A		A	A	A
498	A	A	A	A	A	A	A	A		A	A	A
499	A	A	A	A	A	A	A	A		A	A	A
500	A	A	A	A	A	A	A	A		A	A	A
501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
511	A	A	A	A	A	A	A	A		A	A	A
512												

Fig. 7.2 cont.

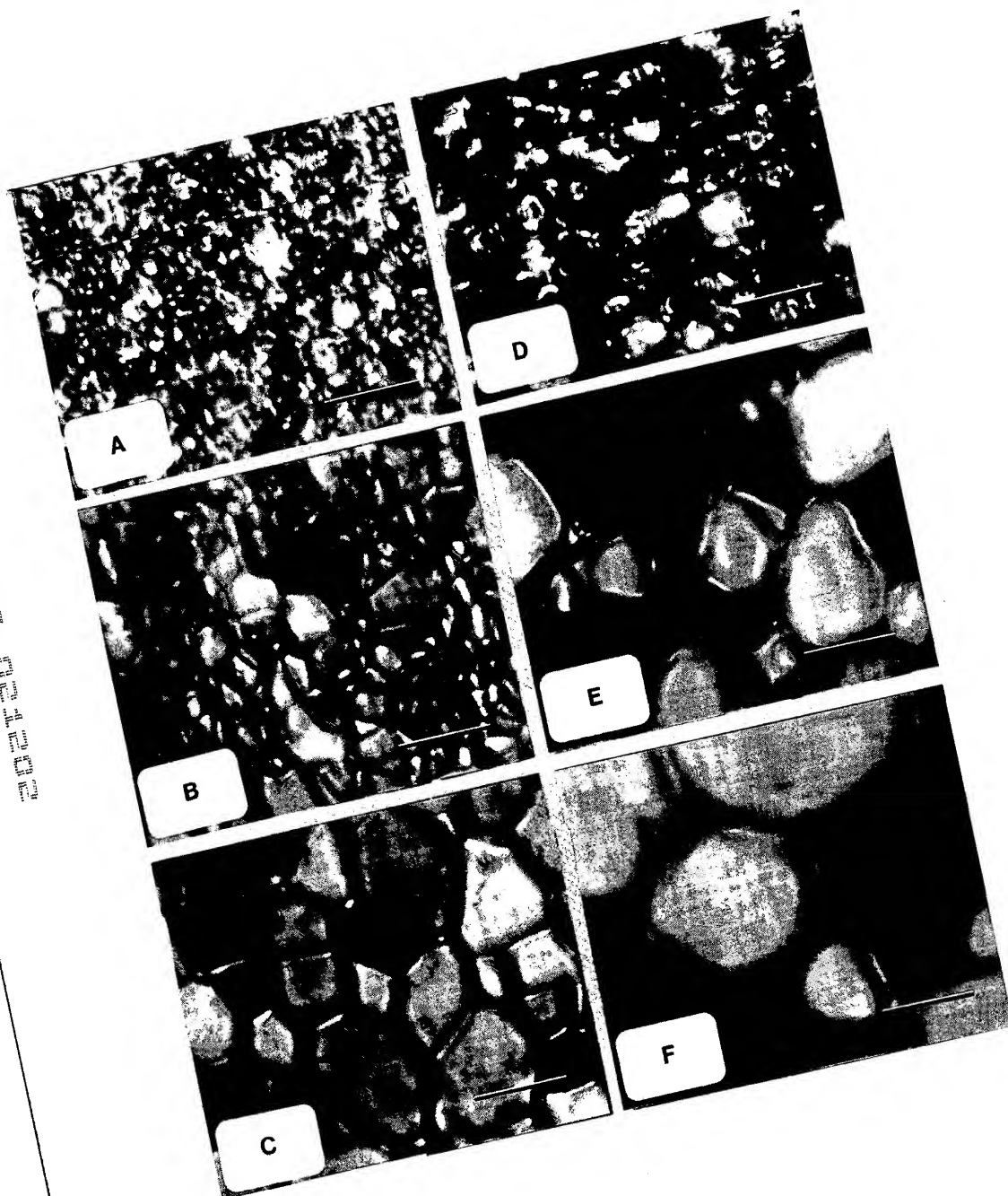
Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus Tm 12.84	Tm 13.17	Consensus to Tm 13.17	Tm P-81	Tm P-82	Consensus Tm P-82	Tm AFP-3	Consensus	GENERAL CONSENSUS	SUBSTITUTIONS - most to least common
1	M	M	M	M	M	M	M	K	L	L	HY*, ALP/SUL	M	M OR GAP	M	
2	K	K	K	K	K	K	K	K	L	L	K OR GAP	K	K OR GAP	K	
3	L	L	L	L	L	L	L	L	L	L	L OR GAP	L	L OR GAP	L	
4	L	L	L	L	L	L	L	L	L	L	L OR GAP	L	L OR GAP	L	
5	L	L	L	L	L	L	L	L	L	L	L OR GAP	L	L OR GAP	L	
6	F	F	F	F	F	F	F	C	C	C	HY*, ALP/SUL OR GAP	C	C OR GAP	C	C
7	F	F	F	F	F	F	F	C	C	C	HY*, AROALP	L	HY*, AROALP	L	L
8	F	F	F	F	F	F	F	C	C	C	HY*, AROALP	L	HY*, AROALP	L	L
9	F	F	F	F	F	F	F	C	C	C	HY*, AROALP	L	HY*, AROALP	L	L
10	A	A	A	A	A	A	A	ALP	ALP	ALP	ALP	L	ALP	L	L
11	A	A	A	A	A	A	A	ALP	ALP	ALP	ALP	L	ALP	L	L
12	A	A	A	A	A	A	A	ALP	ALP	ALP	ALP	L	ALP	L	L
13	V	V	V	V	V	V	V	ALP	ALP	ALP	ALP	L	ALP	L	L
14	V	V	V	V	V	V	V	ALP	ALP	ALP	ALP	L	ALP	L	L
15	G	G	G	G	G	G	G	ALP	ALP	ALP	ALP	L	ALP	L	L
16	A	A	A	A	A	A	A	ALP	ALP	ALP	ALP	L	ALP	L	L
17	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
18	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
19	T	T	T	T	T	T	T	T	T	T	T	L	T	L	L
20	T	T	T	T	T	T	T	T	T	T	T	L	T	L	L
21	T	T	T	T	T	T	T	T	T	T	T	L	T	L	L
22	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
23	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
24	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
25	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
26	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
27	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
28	N	N	N	N	N	N	N	N	N	N	N	L	N	L	L
29	N	N	N	N	N	N	N	N	N	N	N	L	N	L	L
30	N	N	N	N	N	N	N	N	N	N	N	L	N	L	L
31	S	S	S	S	S	S	S	S	S	S	S	L	S	L	L
32	S	S	S	S	S	S	S	S	S	S	S	L	S	L	L
33	E	E	E	E	E	E	E	E	E	E	E	L	E	L	L
34	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
35	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
36	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
37	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
38	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
39	S	S	S	S	S	S	S	S	S	S	S	L	S	L	L
40	S	S	S	S	S	S	S	S	S	S	S	L	S	L	L
41	S	S	S	S	S	S	S	S	S	S	S	L	S	L	L
42	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
43	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	L	Q	L	L
44	E	E	E	E	E	E	E	E	E	E	E	L	E	L	L
45	I	I	I	I	I	I	I	I	I	I	I	L	I	L	L
46	D	D	D	D	D	D	D	D	D	D	D	L	D	L	L
47	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
48	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
49	R	R	R	R	R	R	R	R	R	R	R	L	R	L	L
50	T	T	T	T	T	T	T	T	T	T	T	L	T	L	L
51	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
52	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
53	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
54	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
55	D	D	D	D	D	D	D	D	D	D	D	L	D	L	L
56	D	D	D	D	D	D	D	D	D	D	D	L	D	L	L
57	P	P	P	P	P	P	P	P	P	P	P	L	P	L	L
58	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
59	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
60	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
61	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
62	H	H	H	H	H	H	H	H	H	H	H	L	H	L	L
63	H	H	H	H	H	H	H	H	H	H	H	L	H	L	L
64	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L
65	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L
66	F	F	F	F	F	F	F	F	F	F	F	L	F	L	L
67	F	F	F	F	F	F	F	F	F	F	F	L	F	L	L
68	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
69	K	K	K	K	K	K	K	K	K	K	K	L	K	L	L
70	T	T	T	T	T	T	T	T	T	T	T	L	T	L	L
71	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
72	V	V	V	V	V	V	V	V	V	V	V	L	V	L	L
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76	A	A	A	A	A	A	A	A	A	A	A	L	A	L	L
77	A	A	A	A	A	A	A	A	A	A	A	L	A	L	L
78	D	D	D	D	D	D	D	D	D	D	D	L	D	L	L

Fig. 7.3





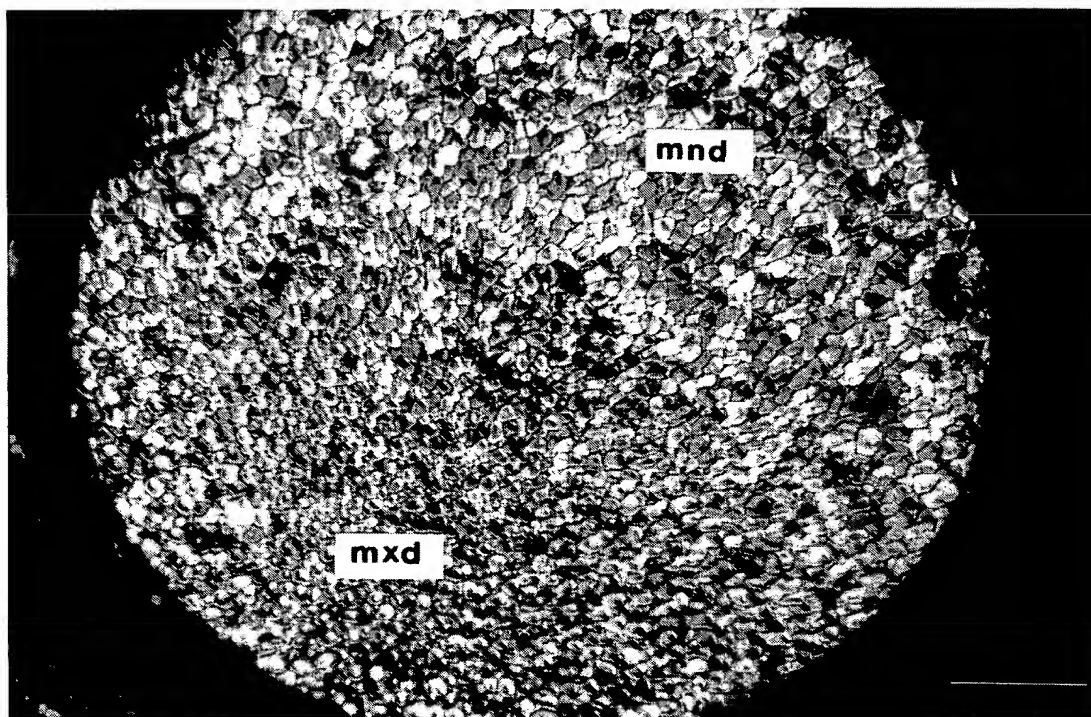
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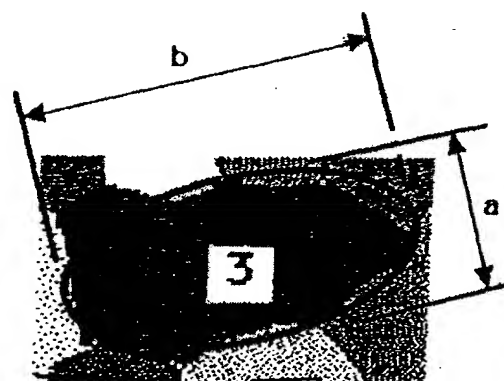
*Fig. 8.0*



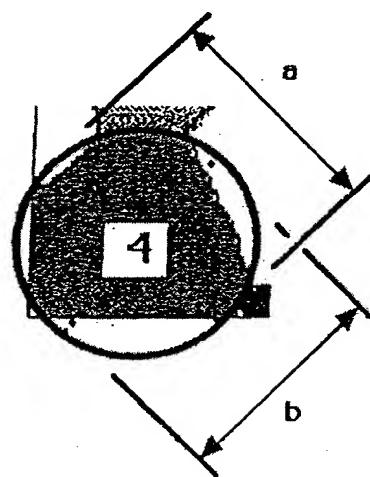
*Fig. 8.1a*



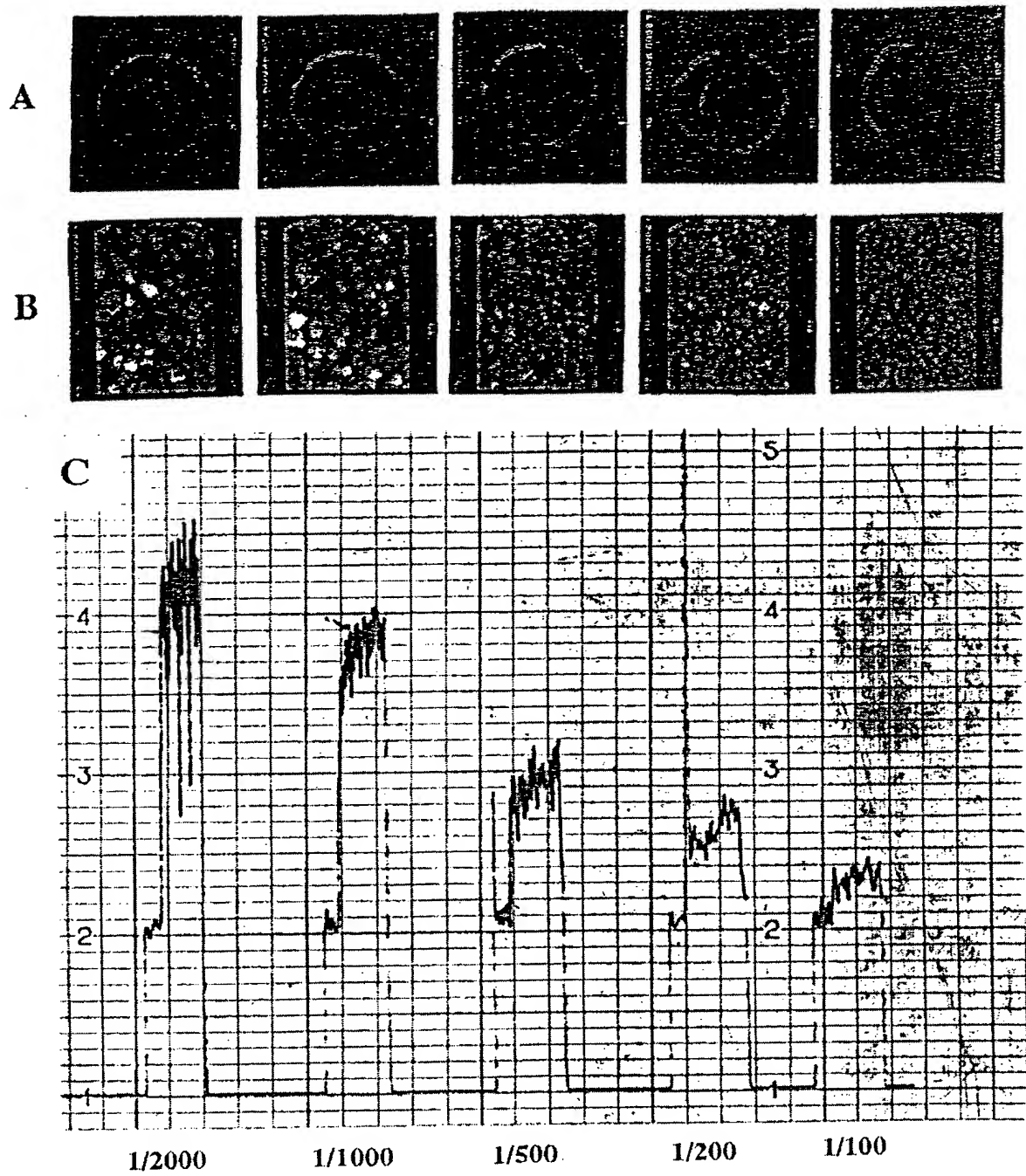
*Fig. 8.1b*



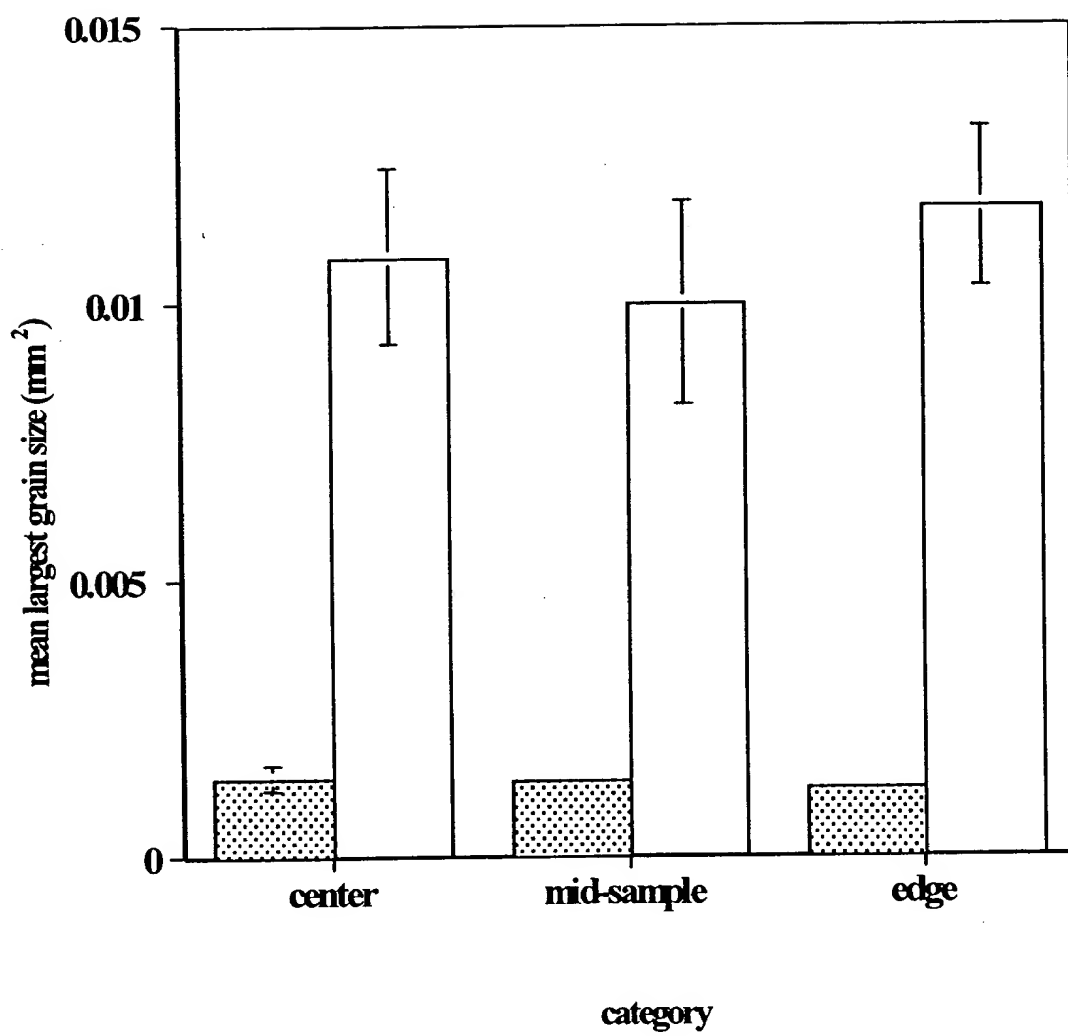
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*Fig. 8.2*

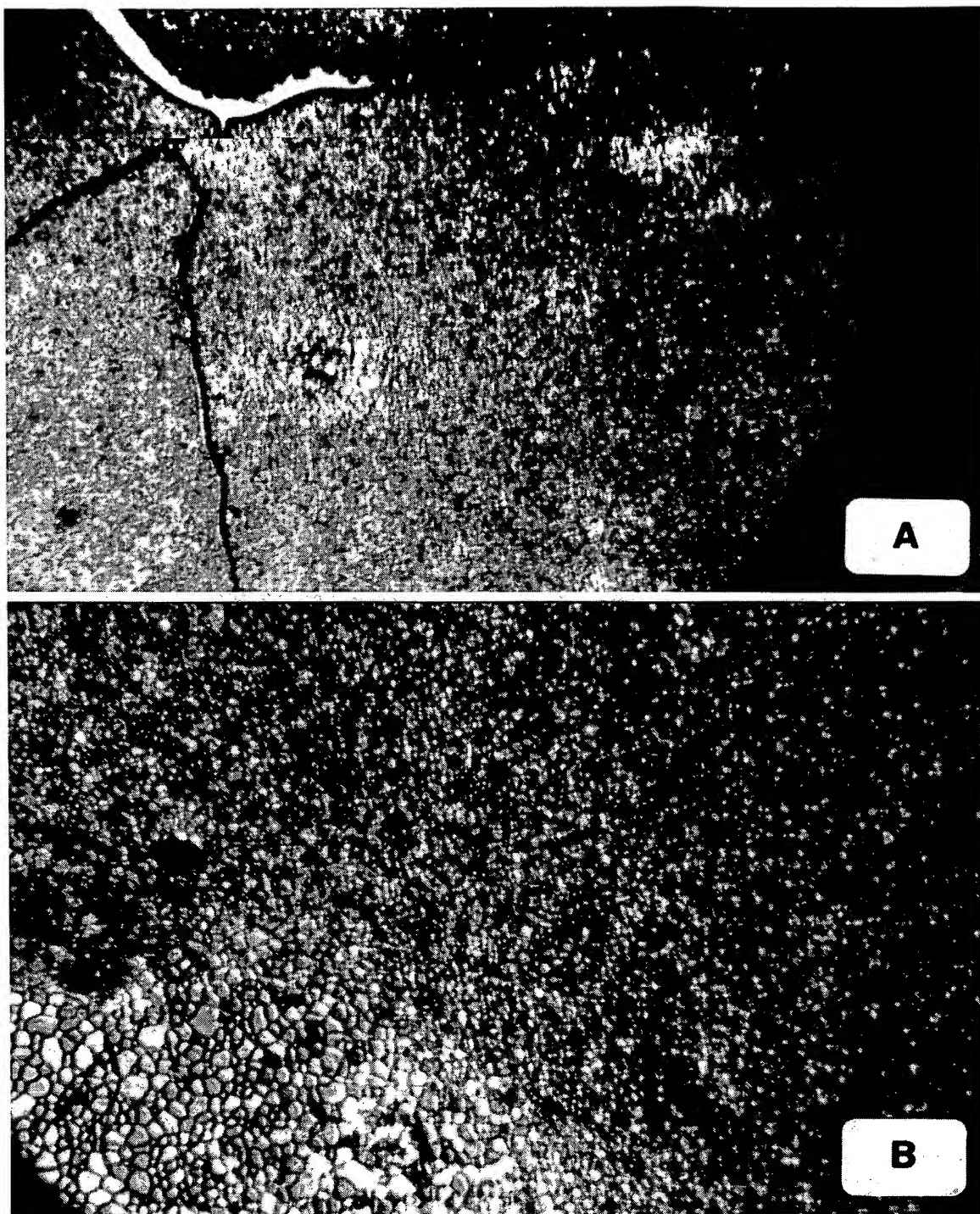


*Fig. 8.3*

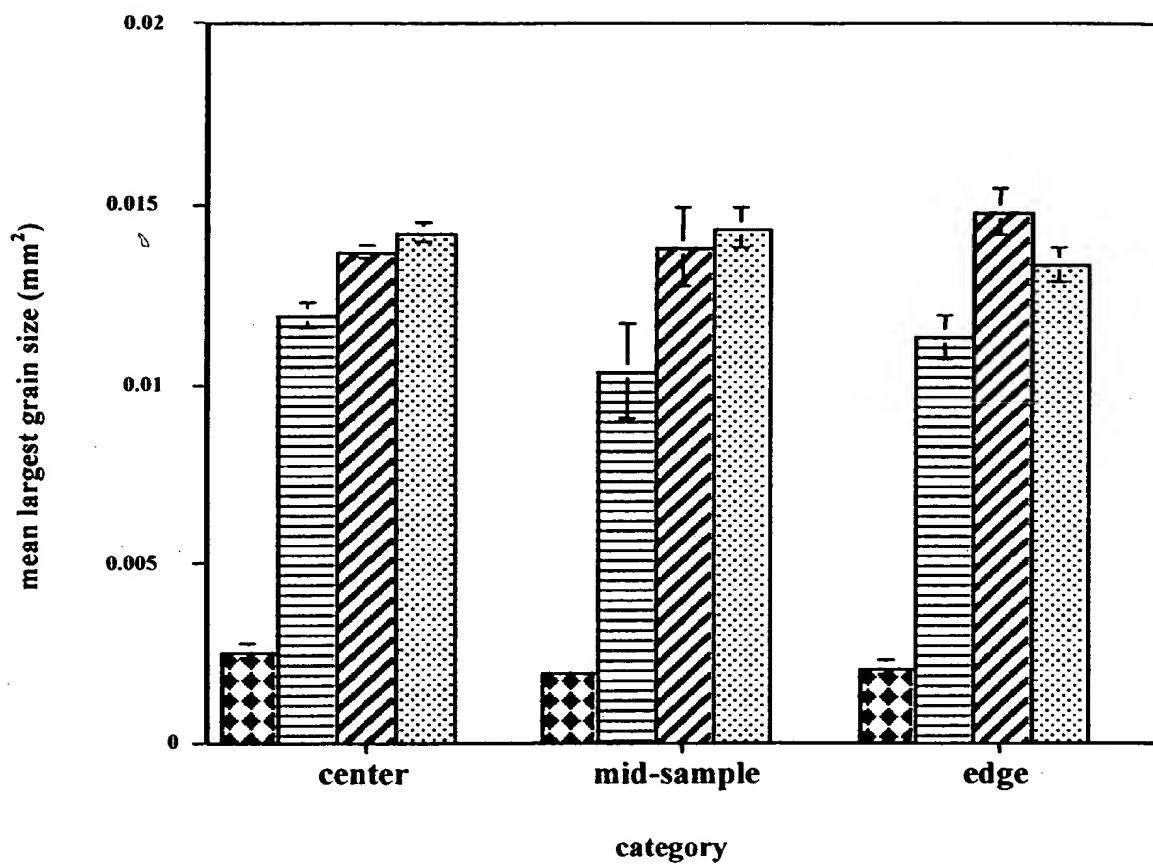


*Fig. 8.4a*

09070750.024.202

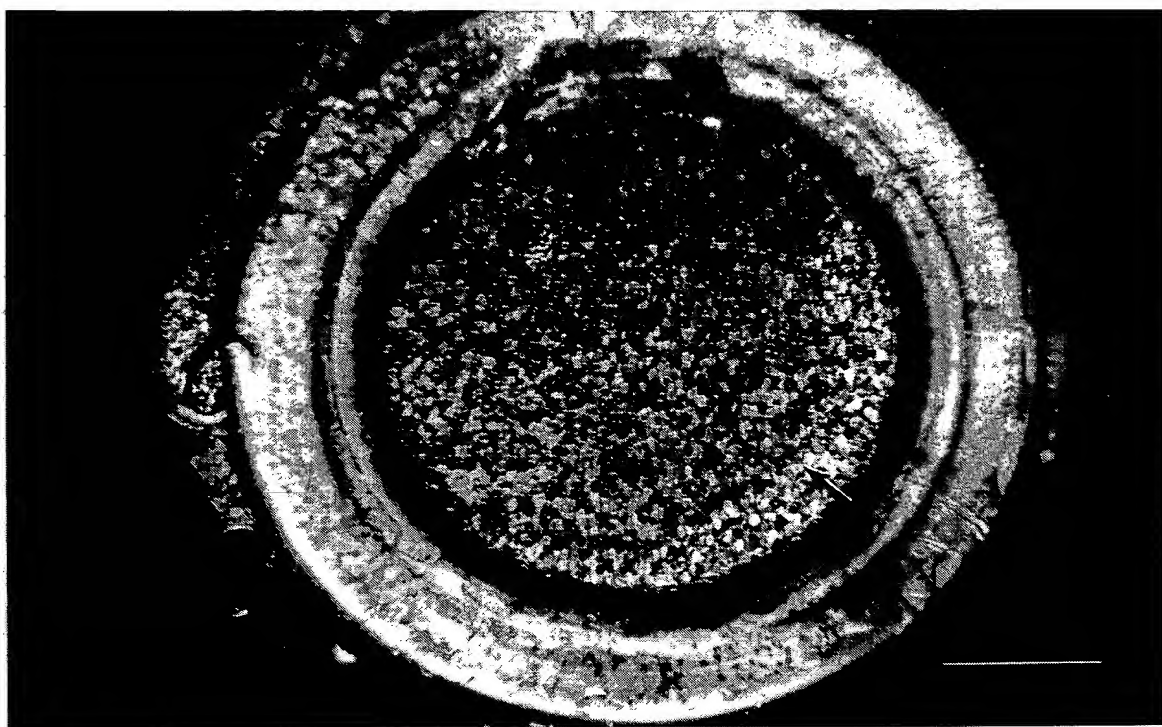


*Fig. 8.4b*

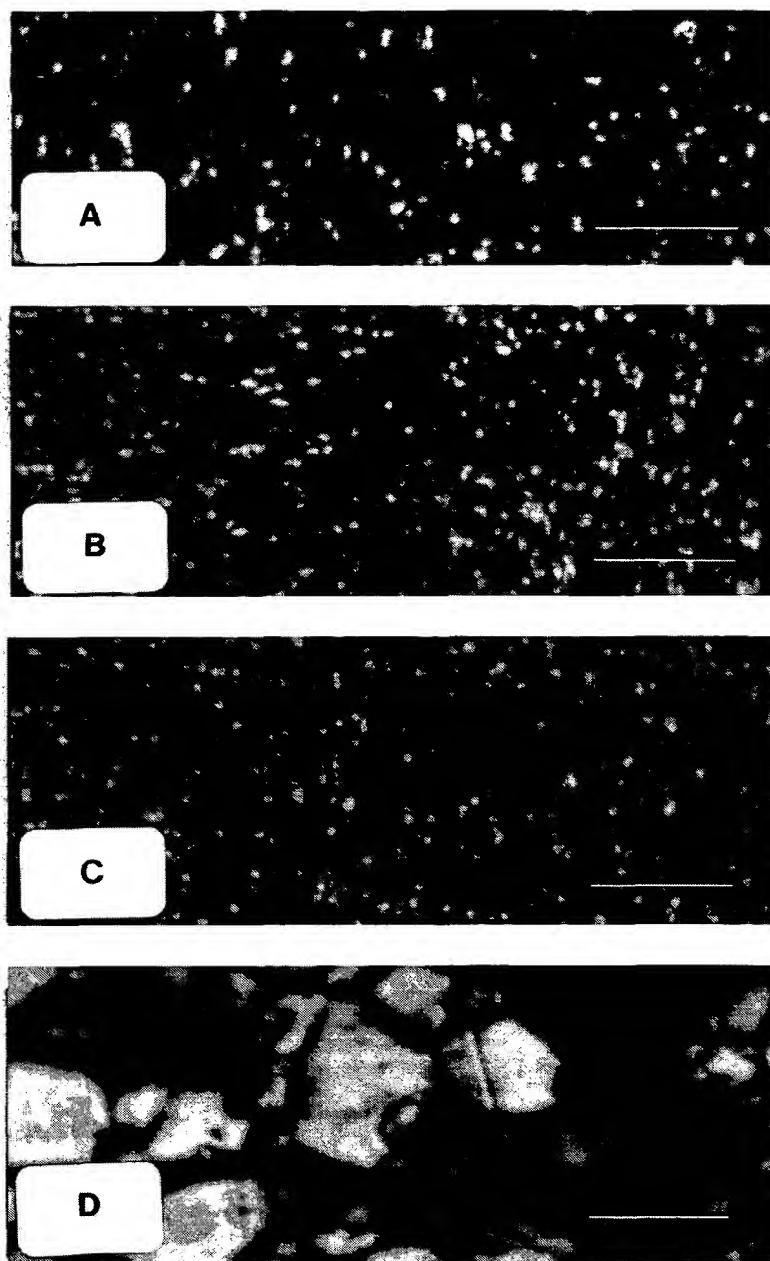


*Fig. 8.5a*

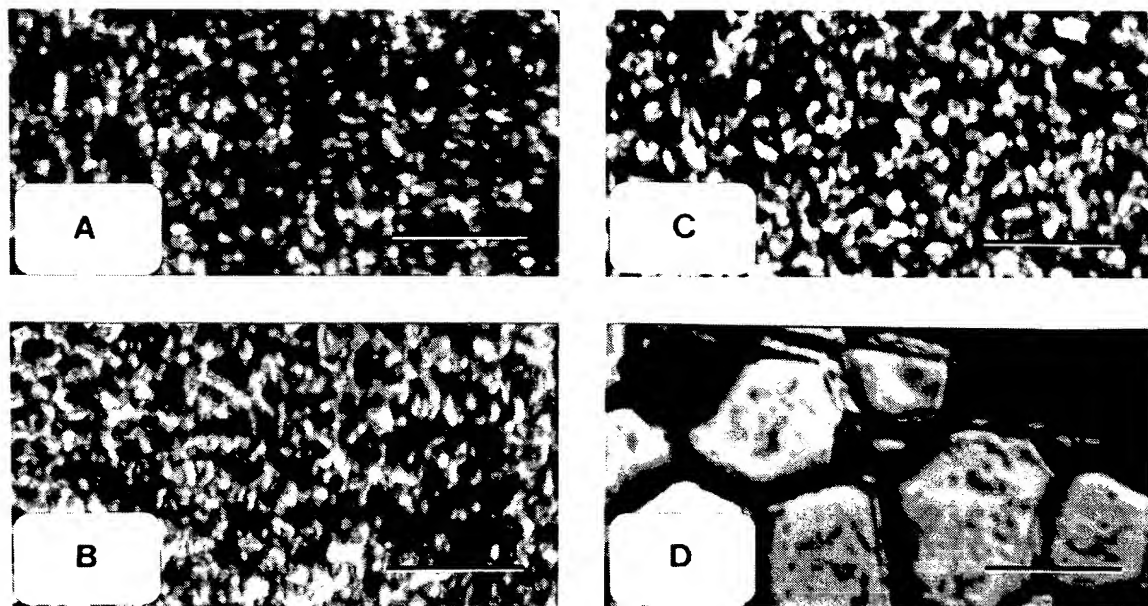




*Fig. 8.5b*



*Fig. 8.6*



*Fig. 8.7*

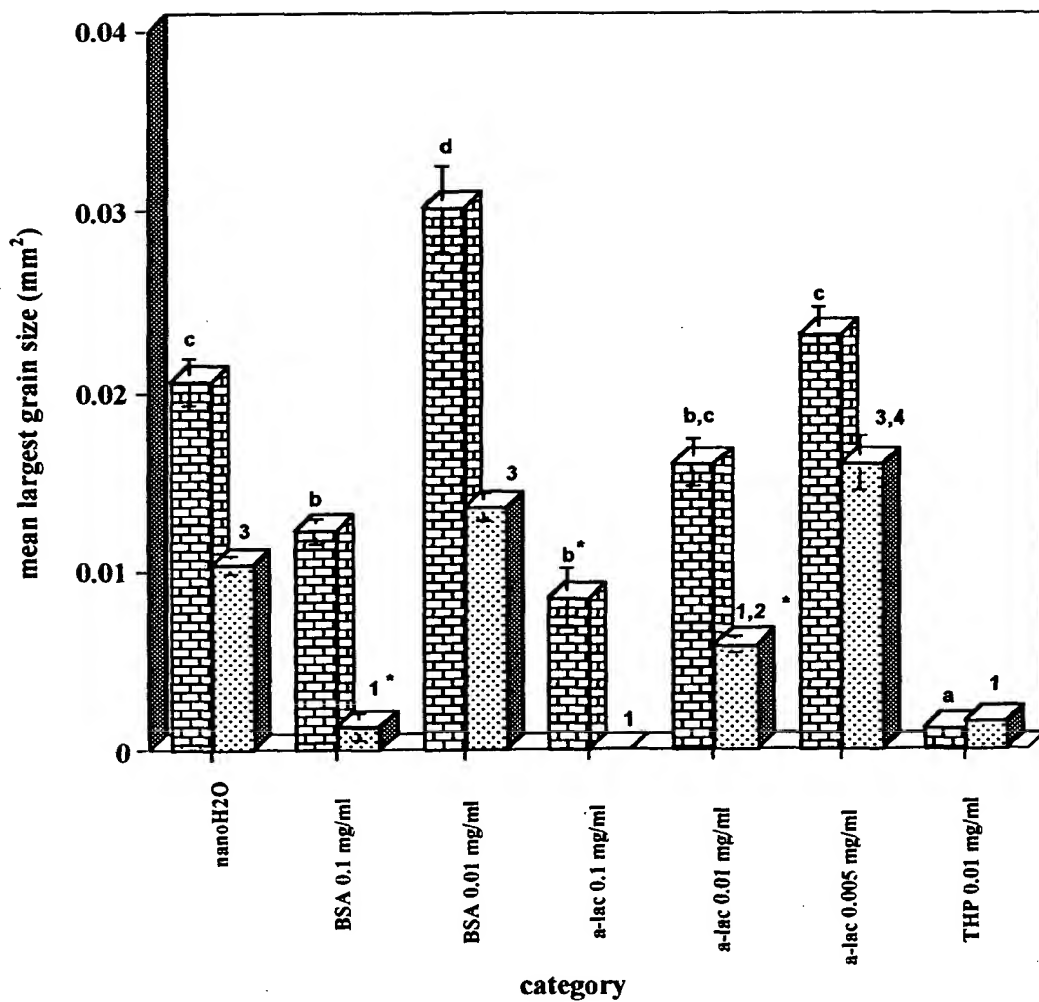
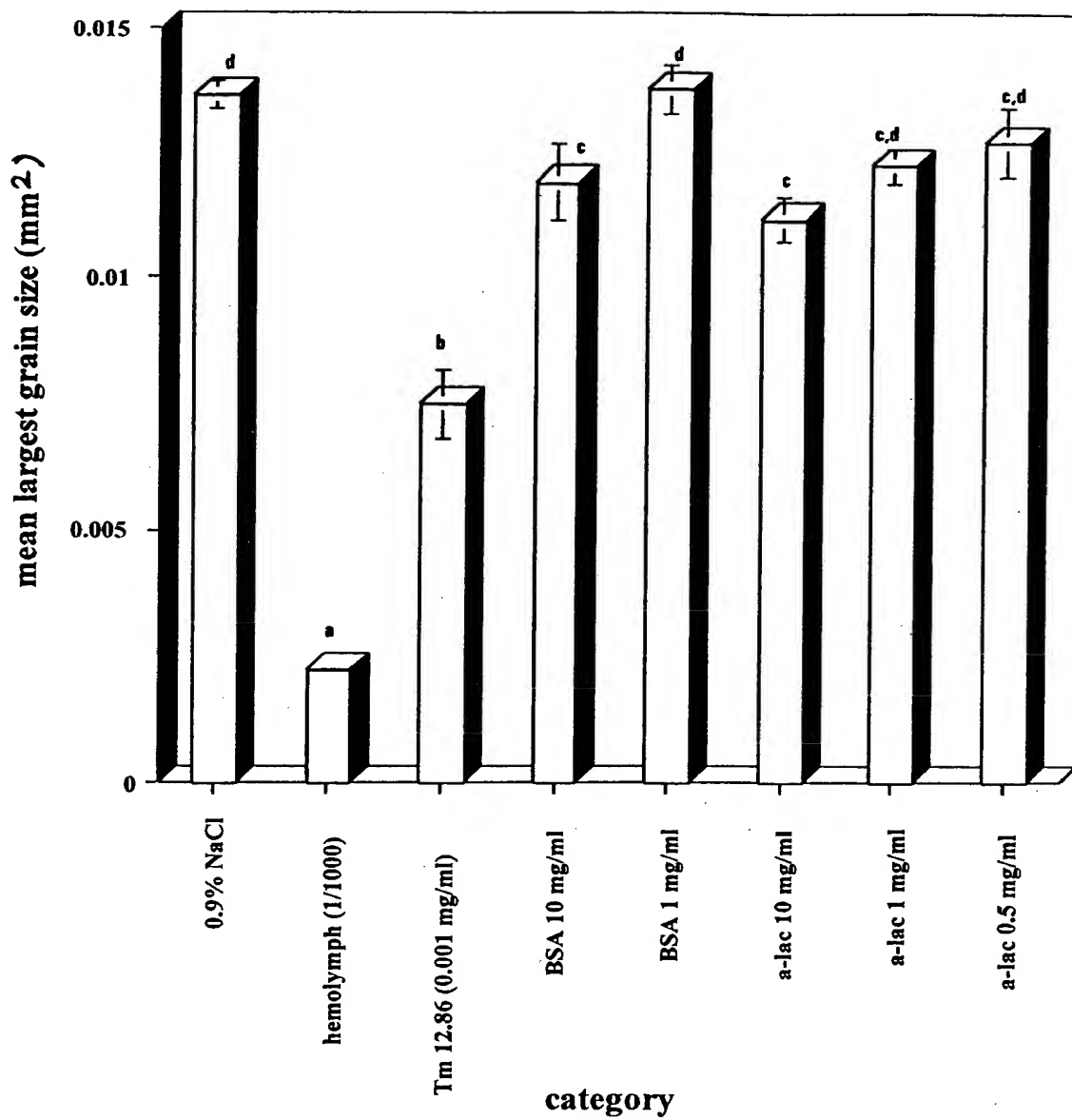
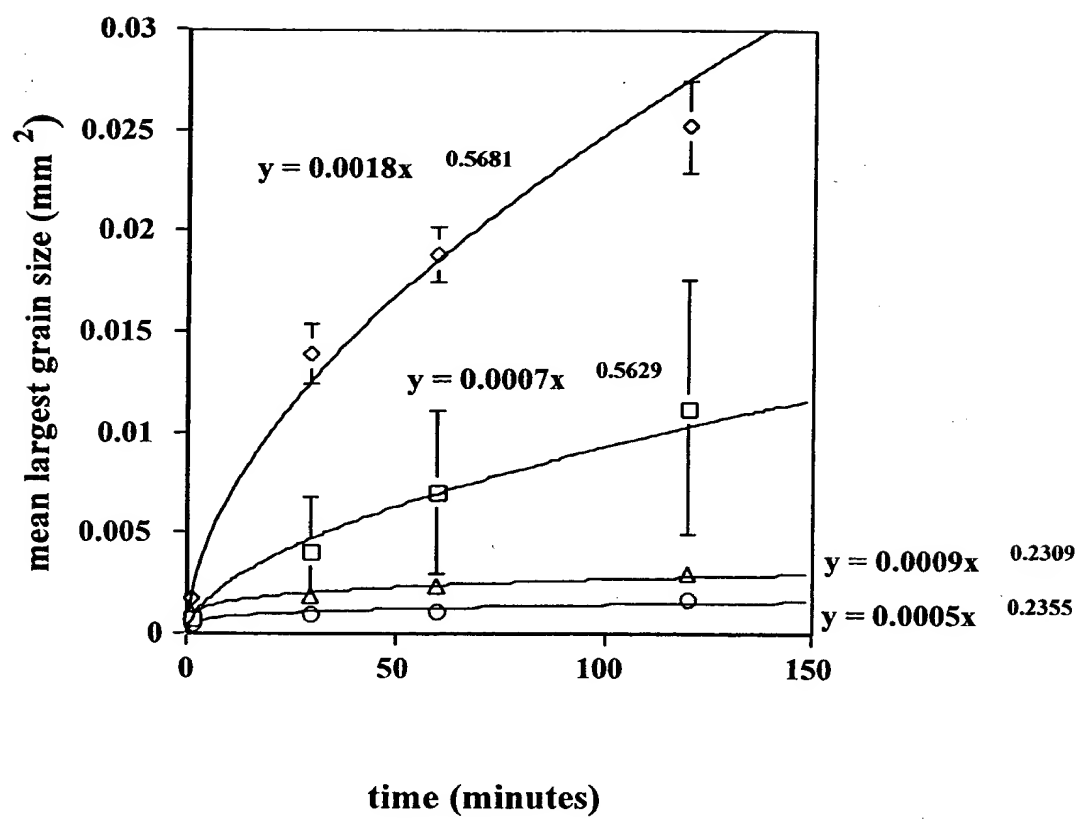


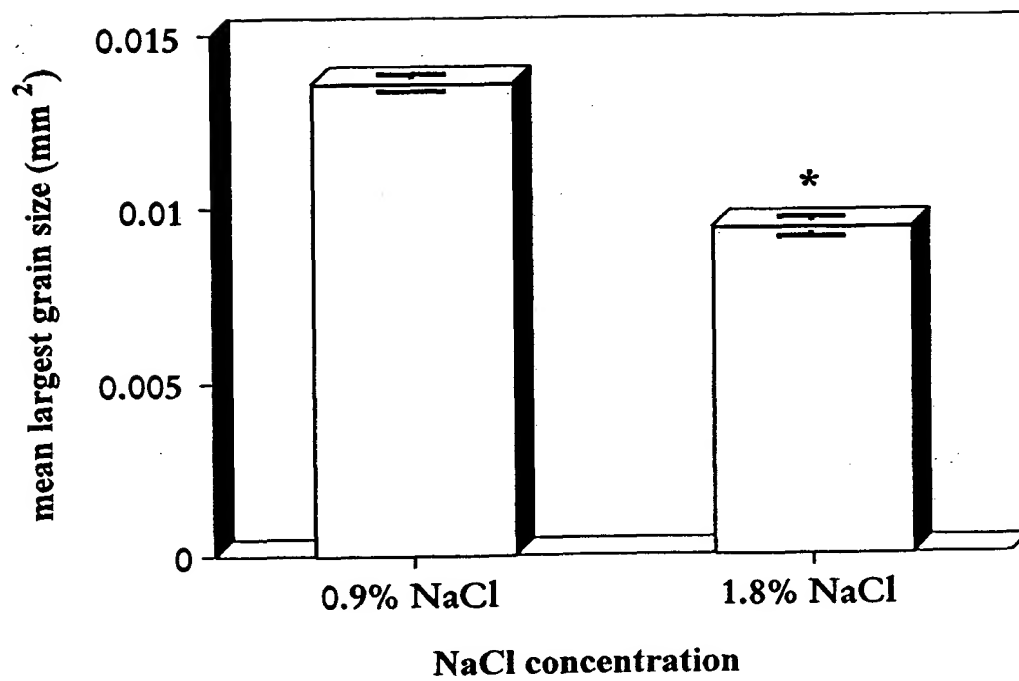
Fig. 8.8



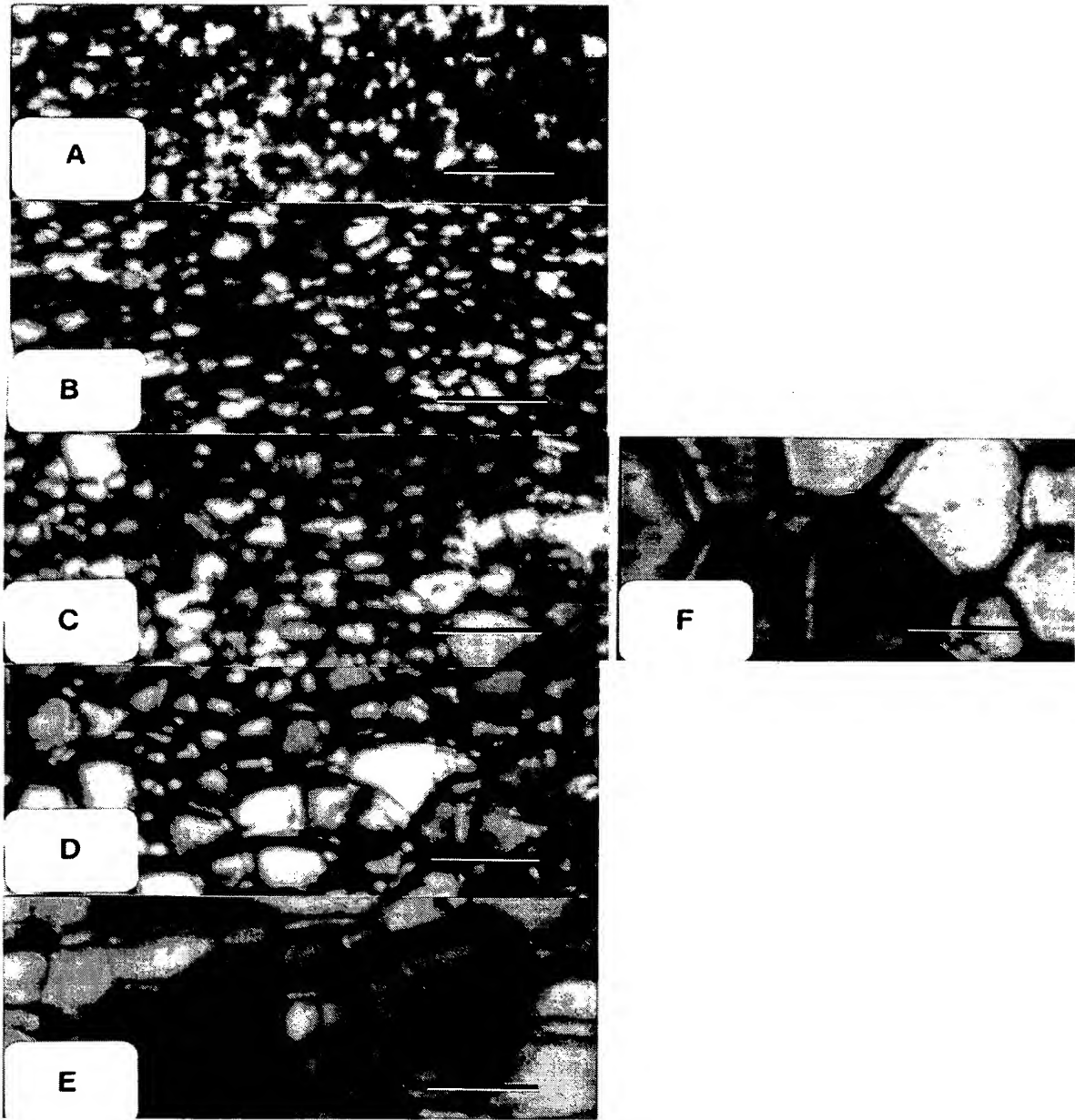
*Fig. 8.9*



*Fig. 8.10*



*Fig. 8.11*



*Fig. 8.12*



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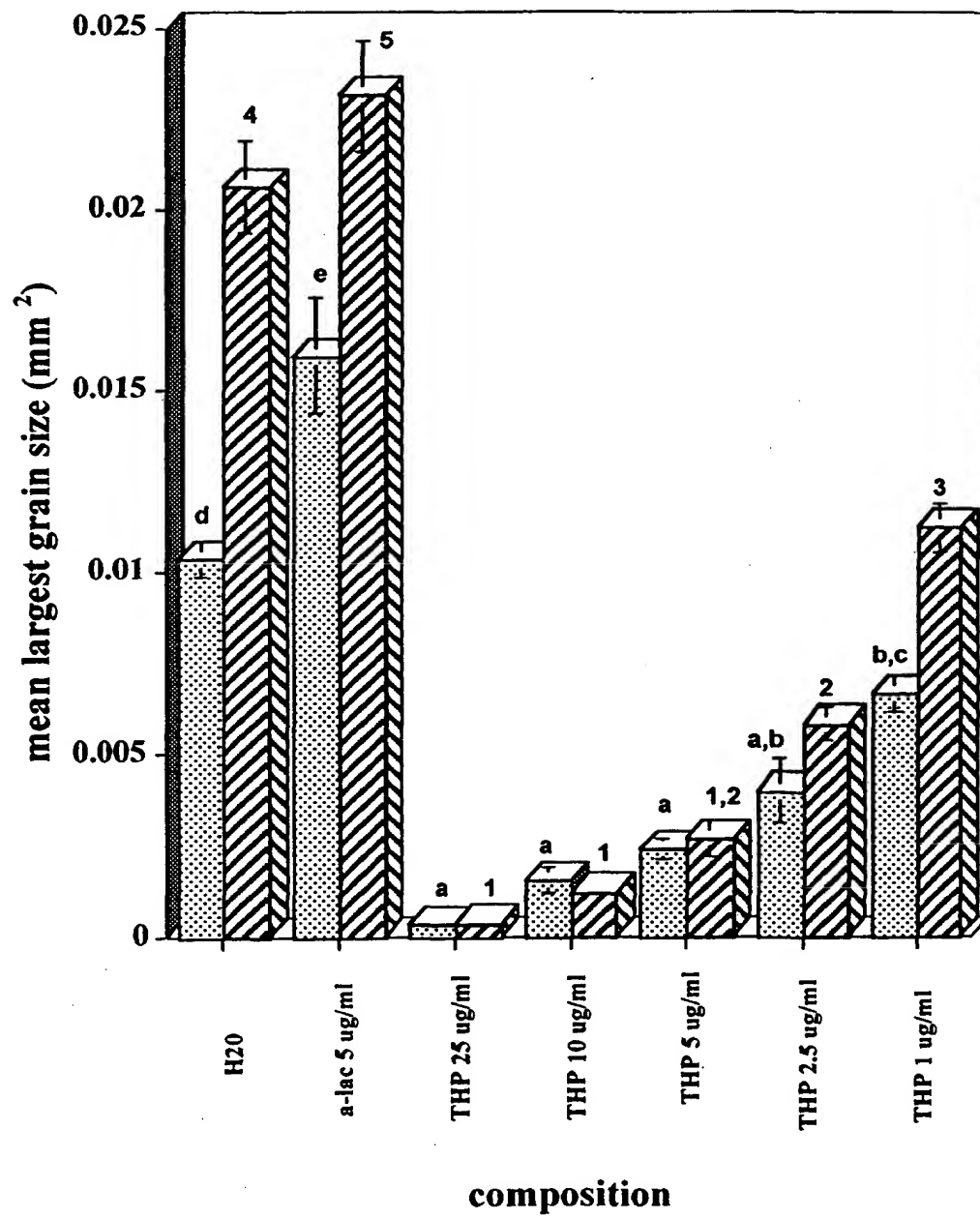
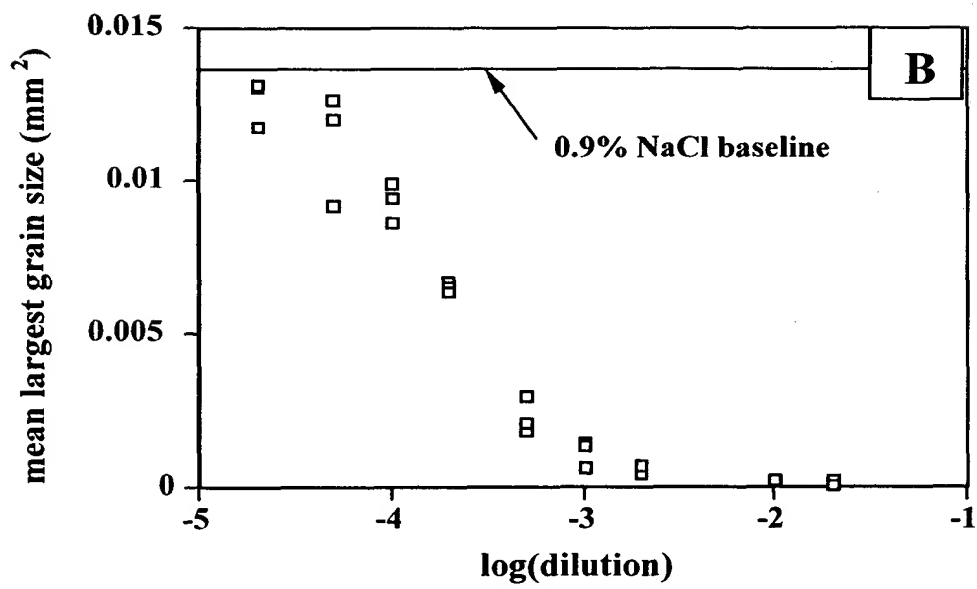
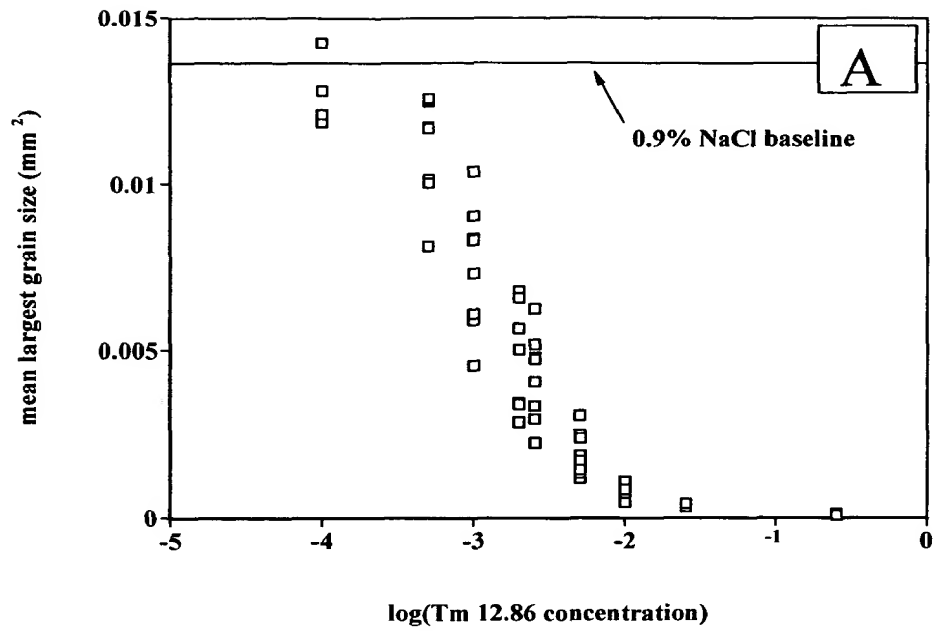


Fig. 8.13

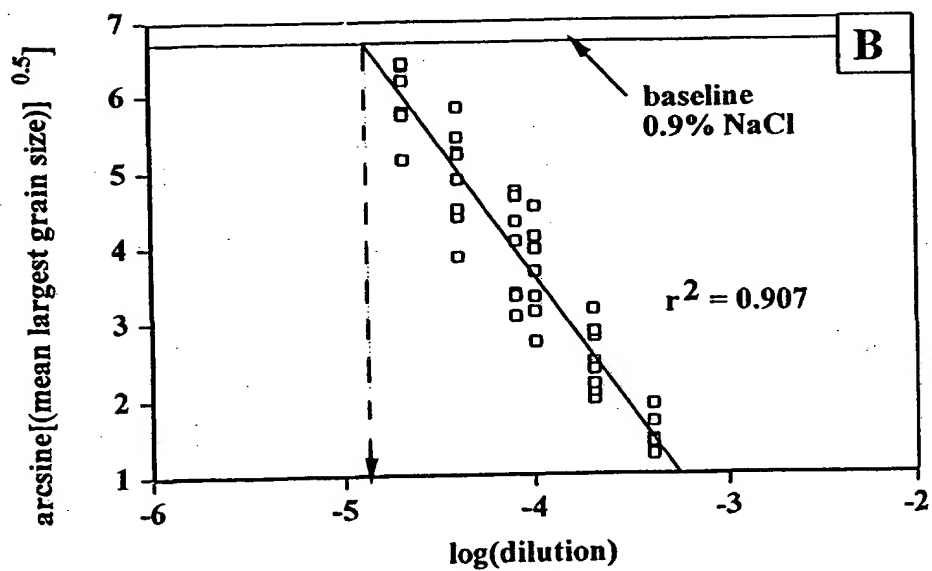
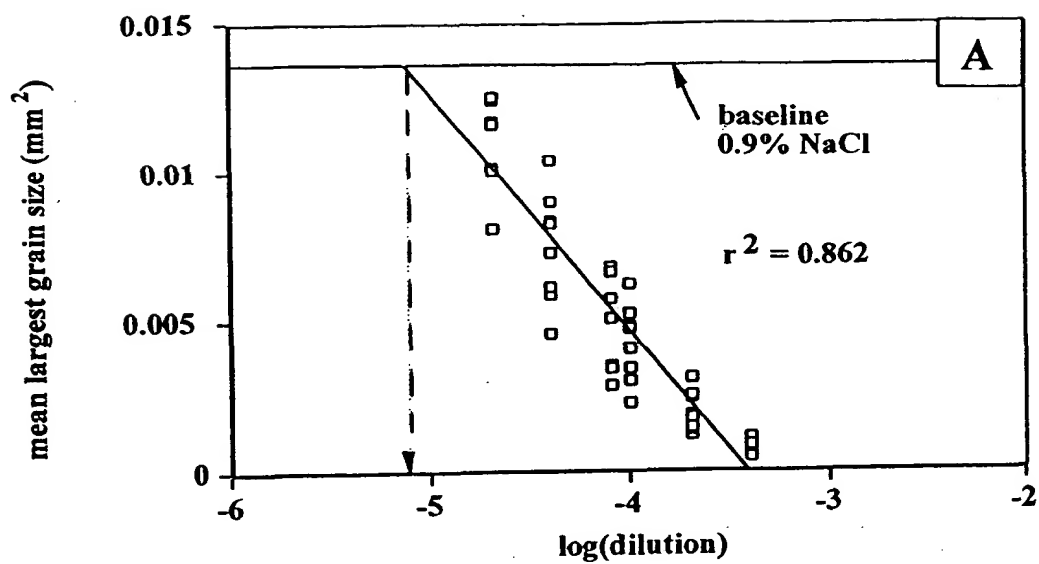
Figure 1 consists of ten scanning electron micrographs (A-J) showing the surface of the larva of the black fly, *Simulium (Simulium) vittatum*. The panels are arranged in two columns. The left column (A-E) shows the head and thorax, while the right column (F-J) shows the abdomen. Each panel includes a scale bar in the bottom right corner.

*Fig. 8.14*

*Fig. 8.15*

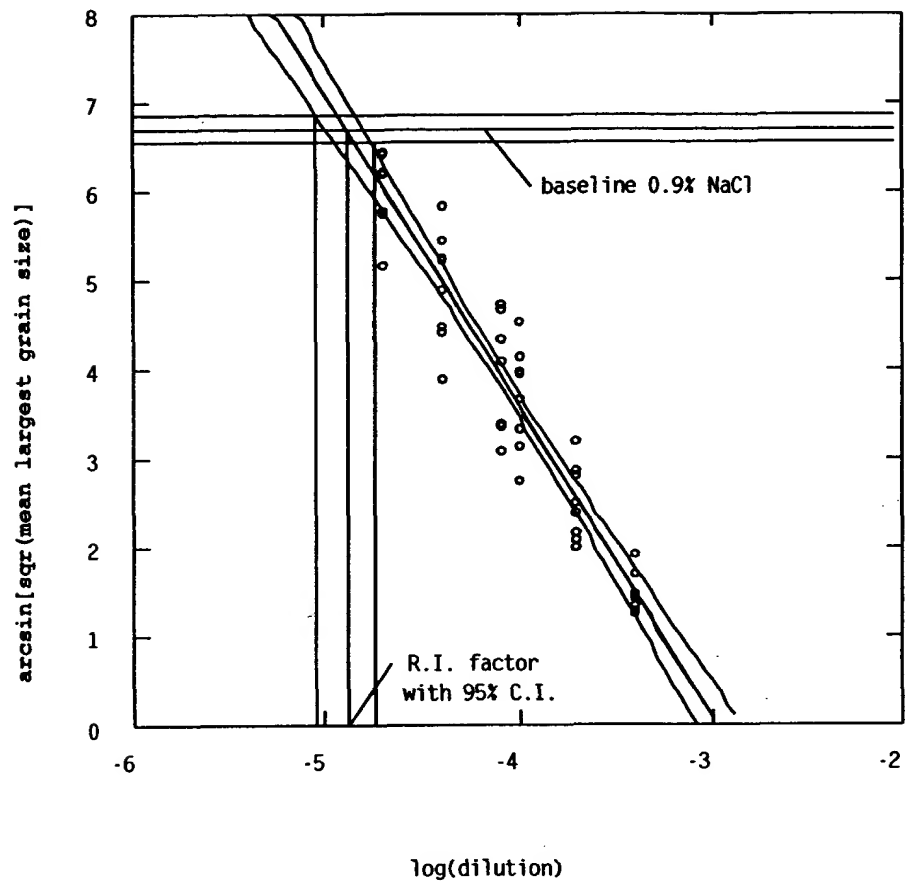


*Fig. 8.16*



*Fig. 8.17*

20250923



*Fig. 8.18*

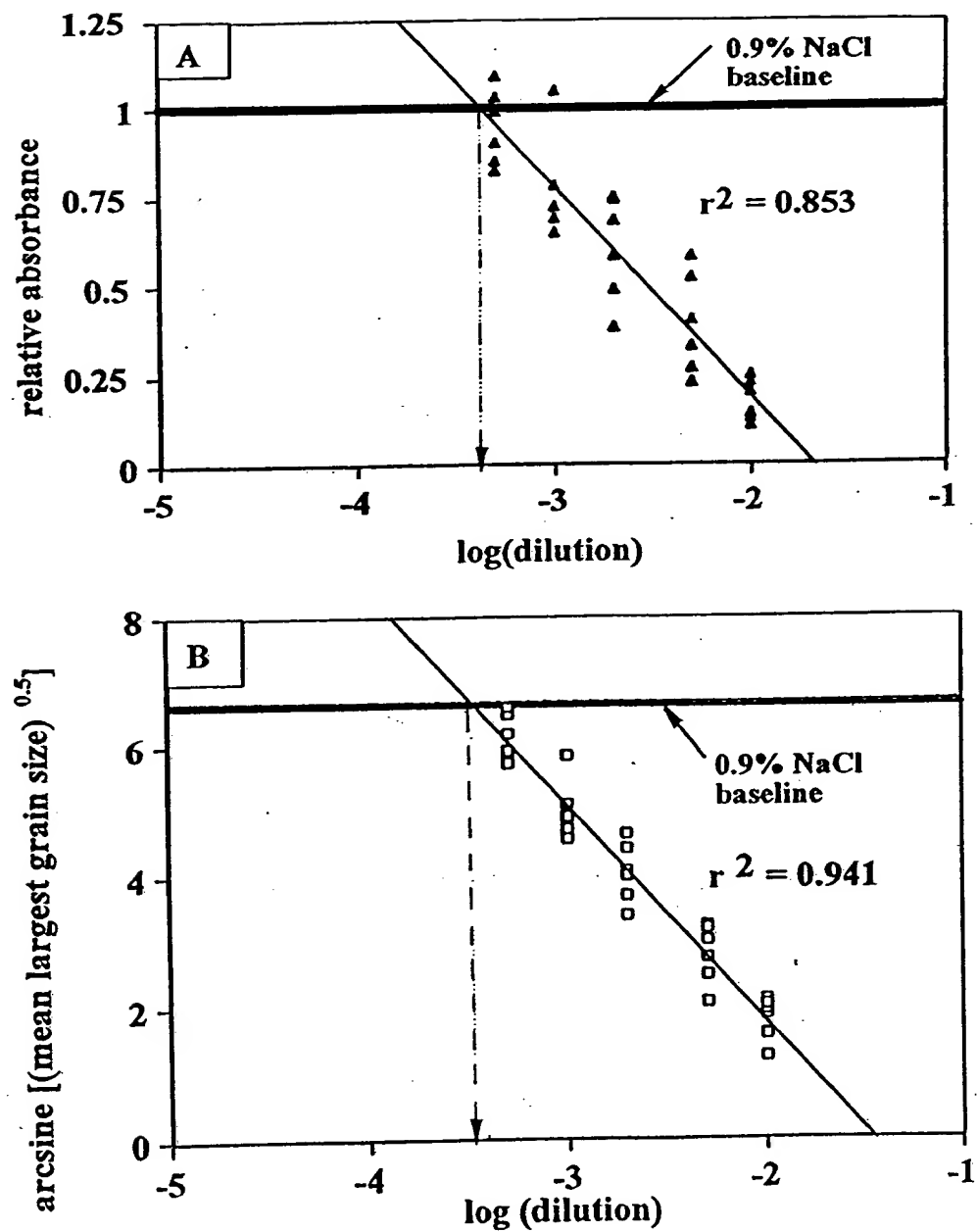


Fig. 8.19

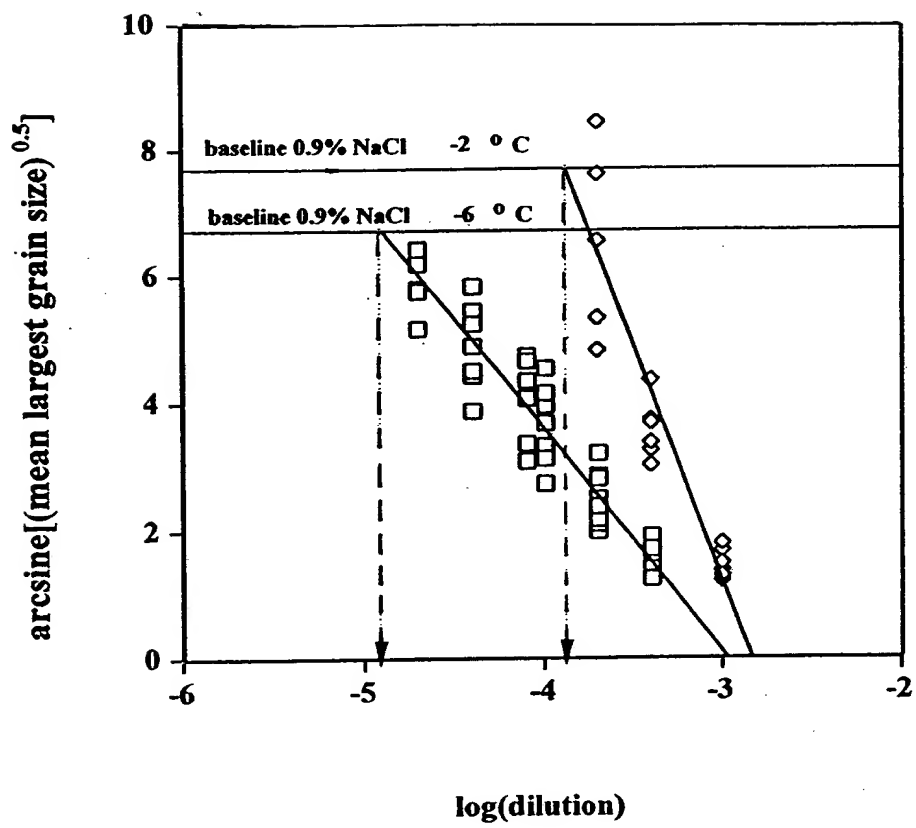


Fig. 8.20



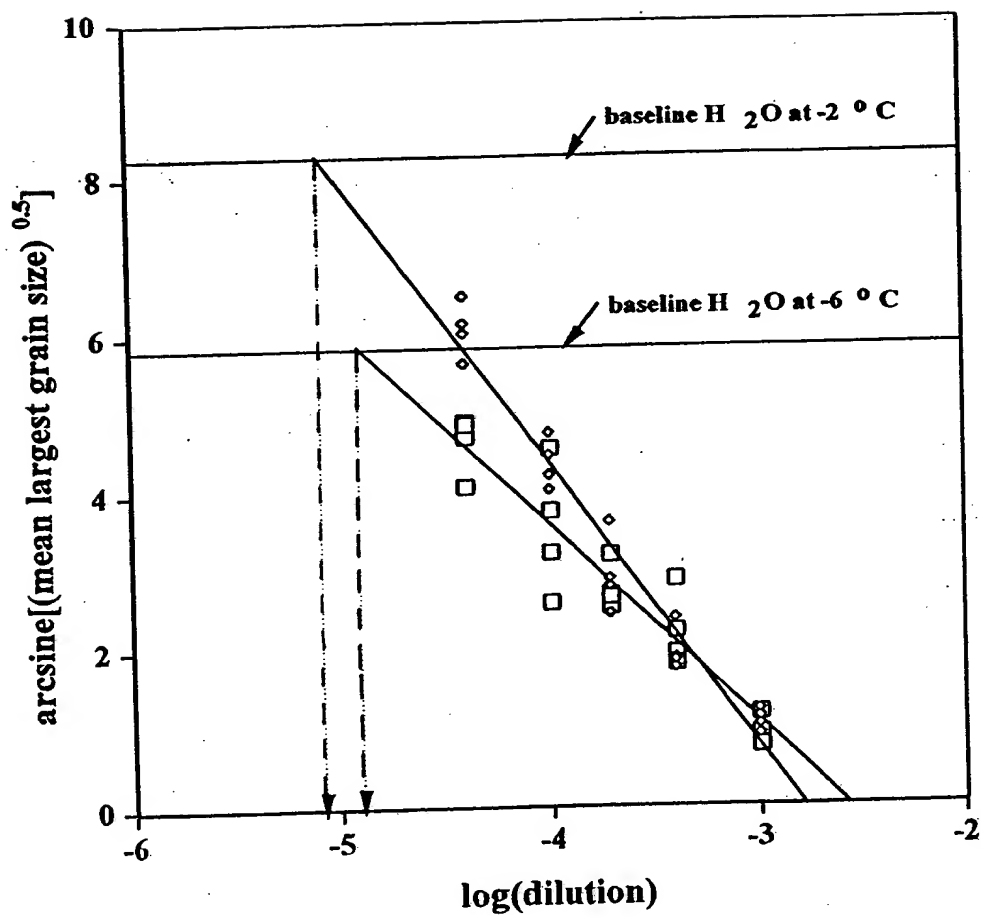


Fig. 8.21

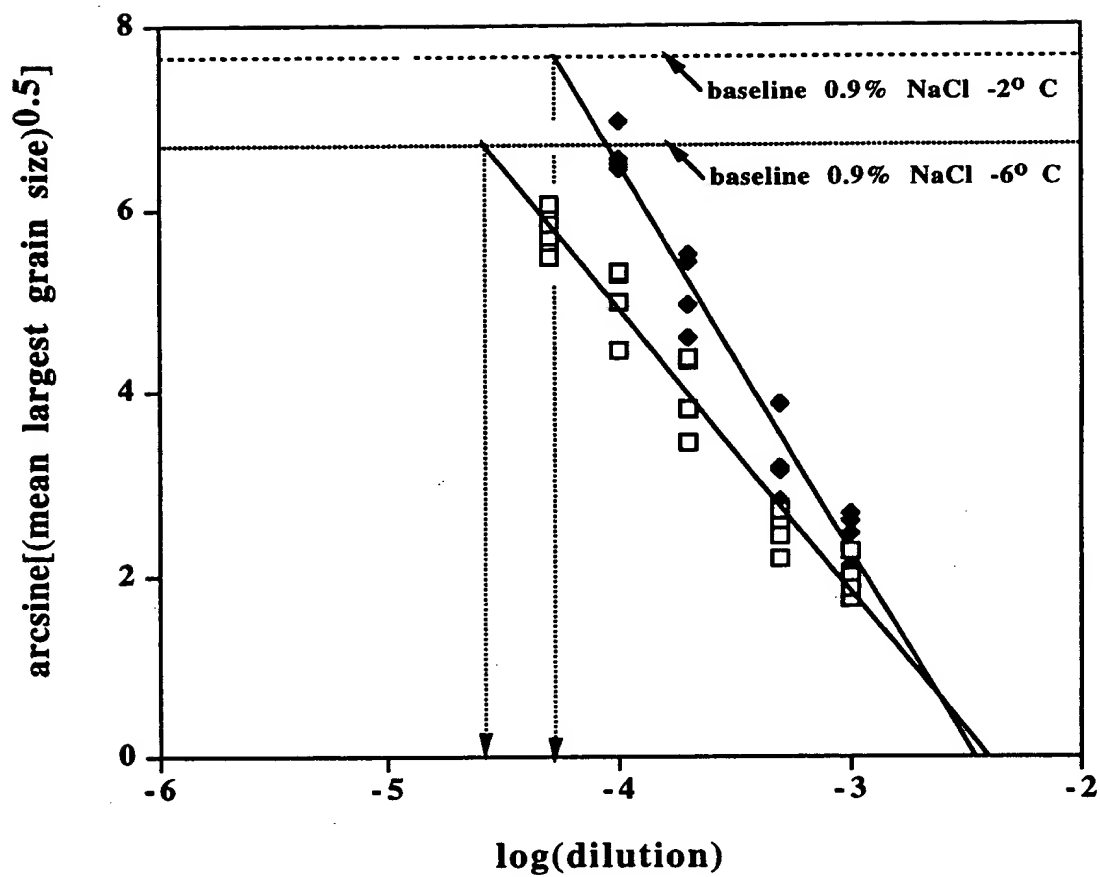


Fig. 8.22

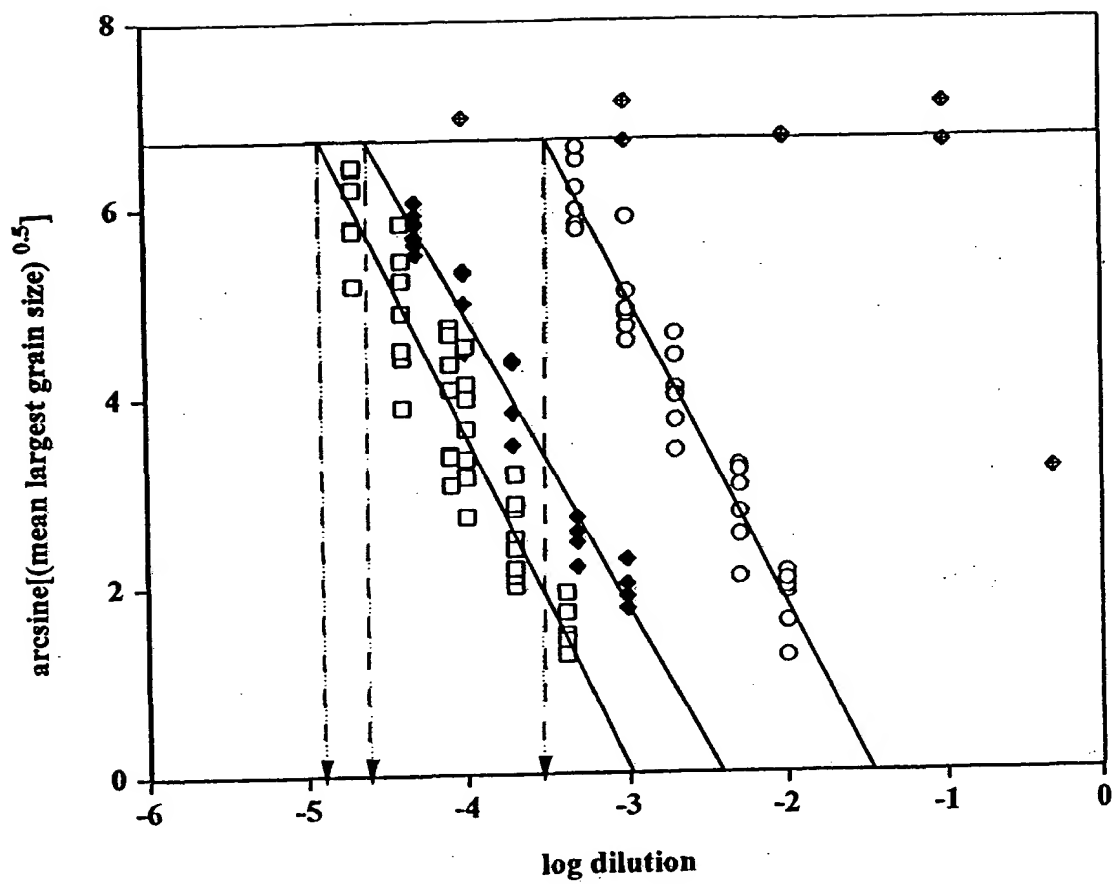


Fig. 8.23

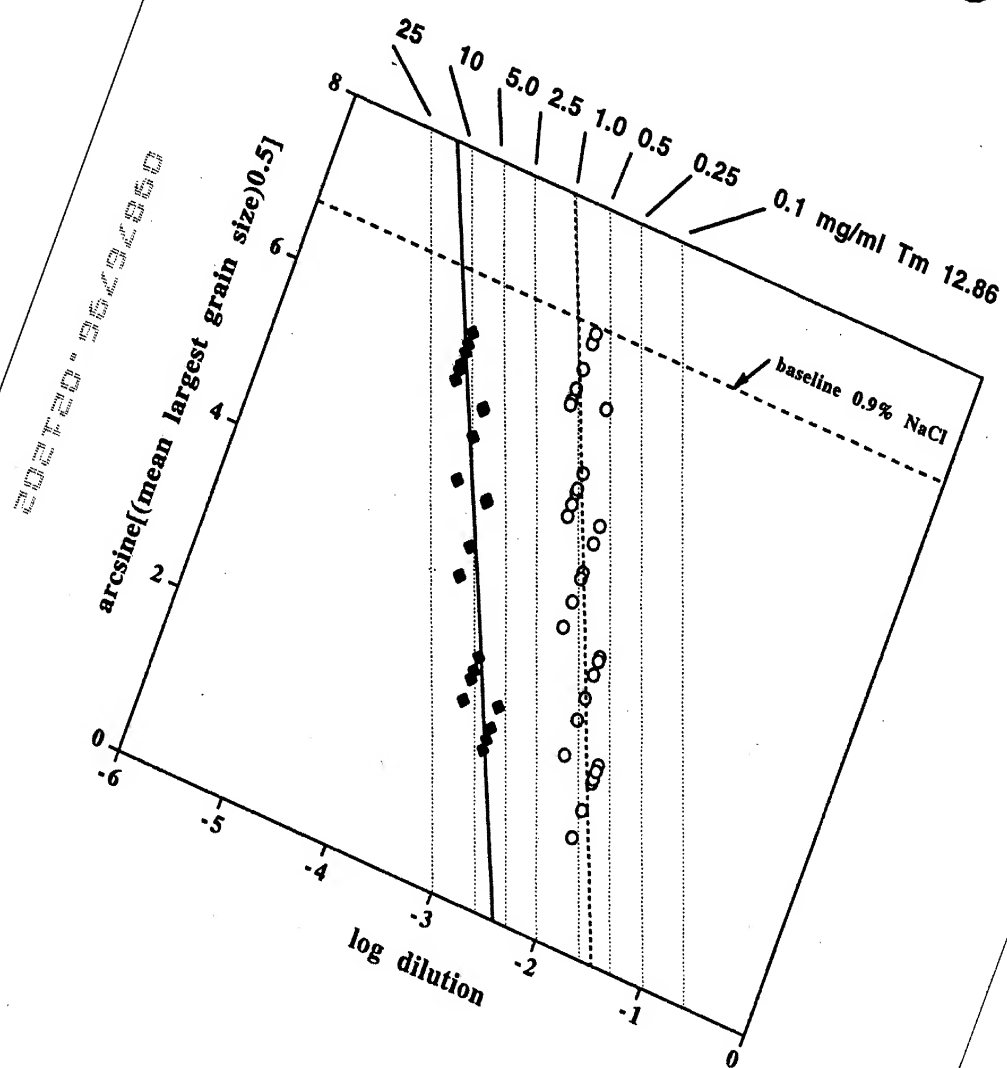
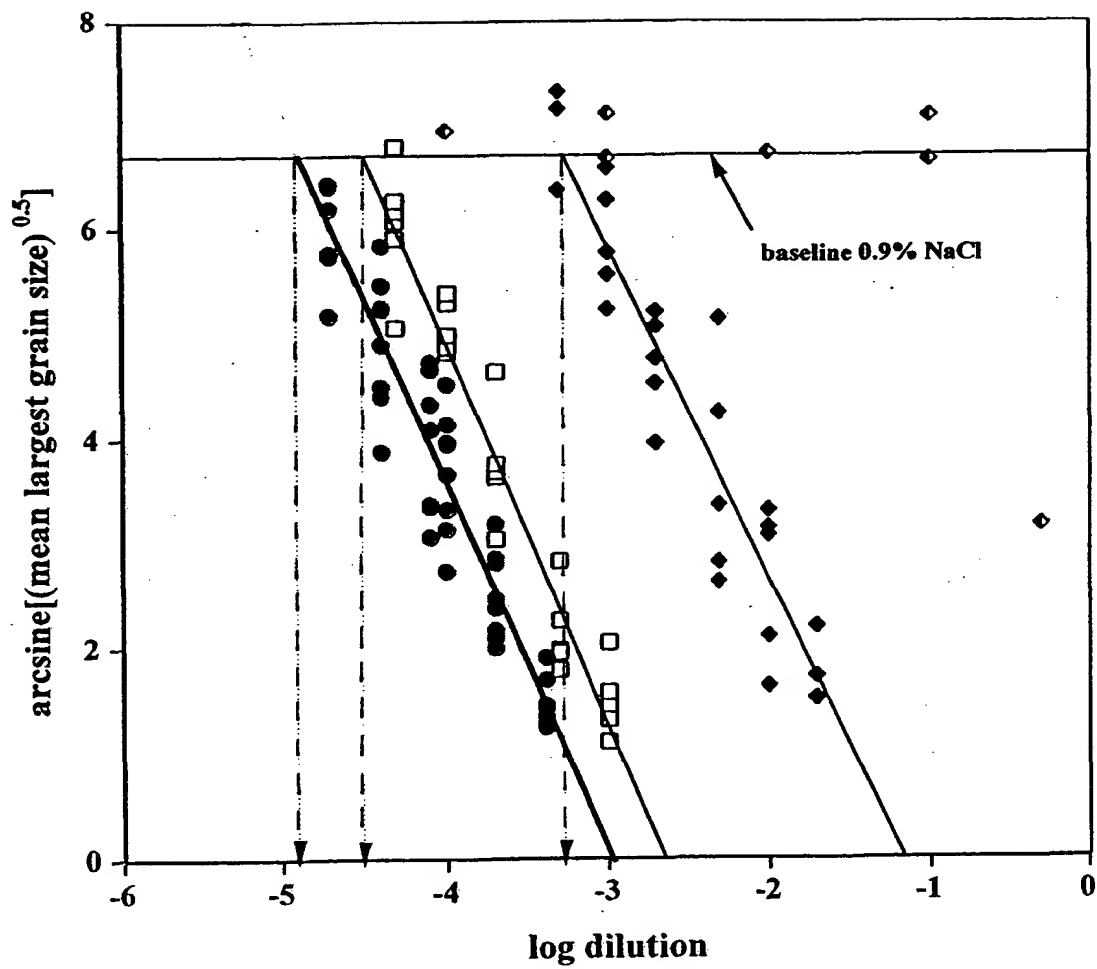


Fig. 8.24

2025-20-95/2/950



*Fig. 8.25*

202720-9629260

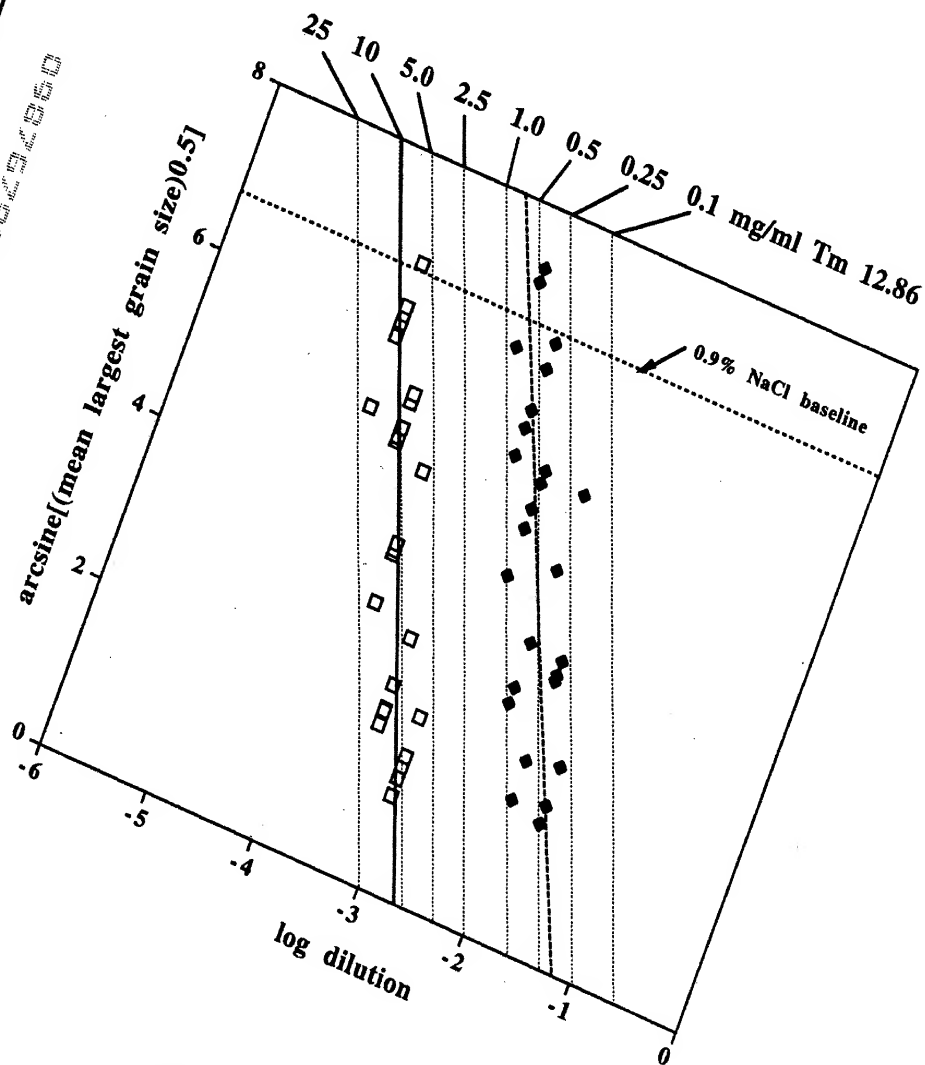


Fig. 8.26

2025-03-26 13:28:50

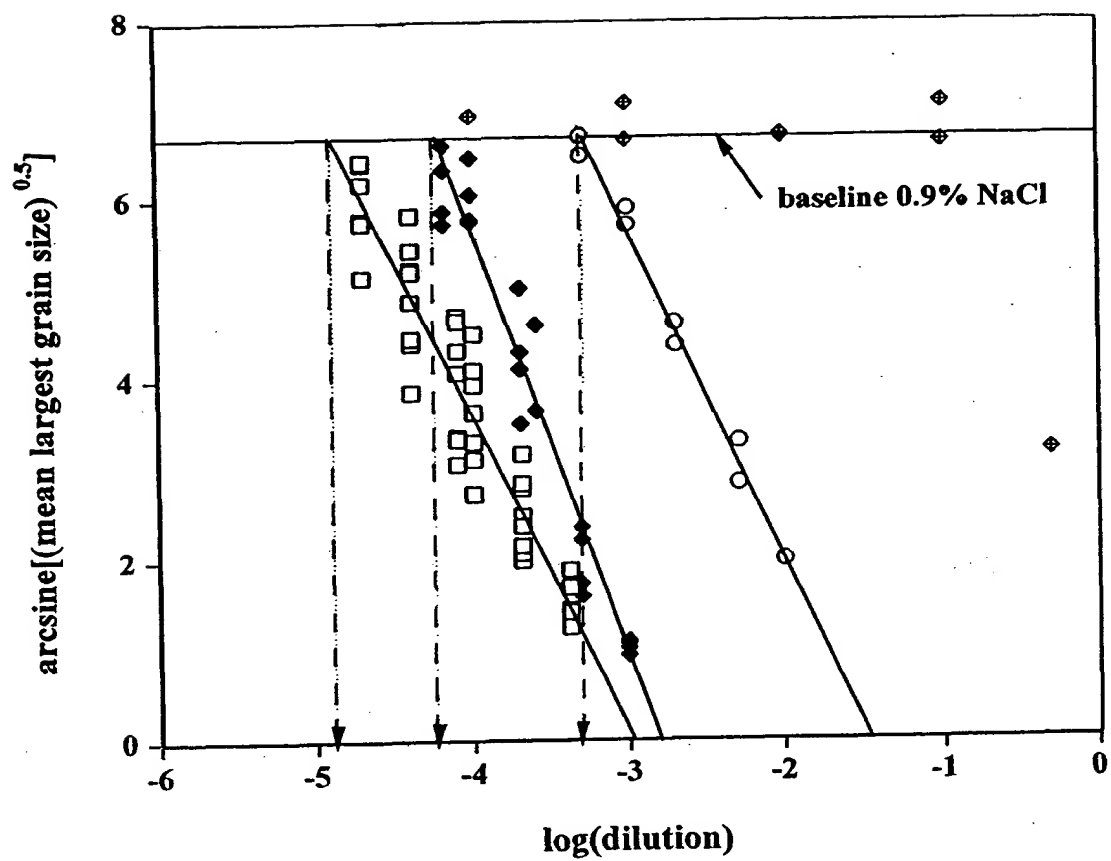


Fig. 8.27

2025-20-195/2050

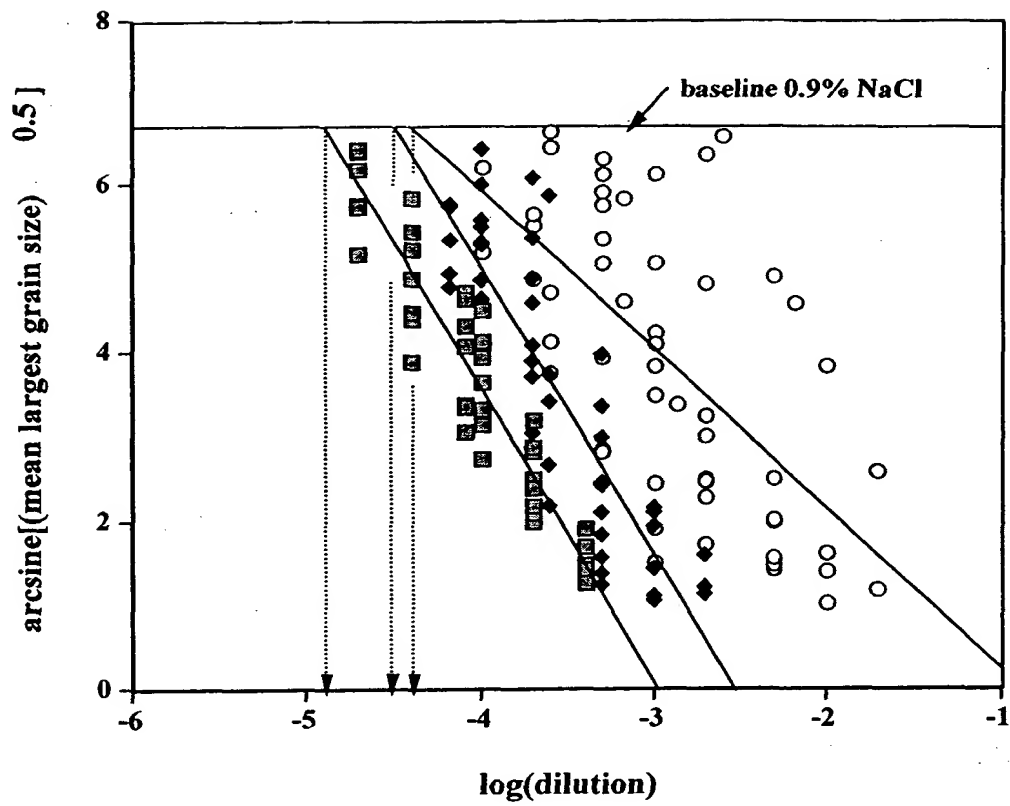


Fig. 8.28



202720 95/09/85B

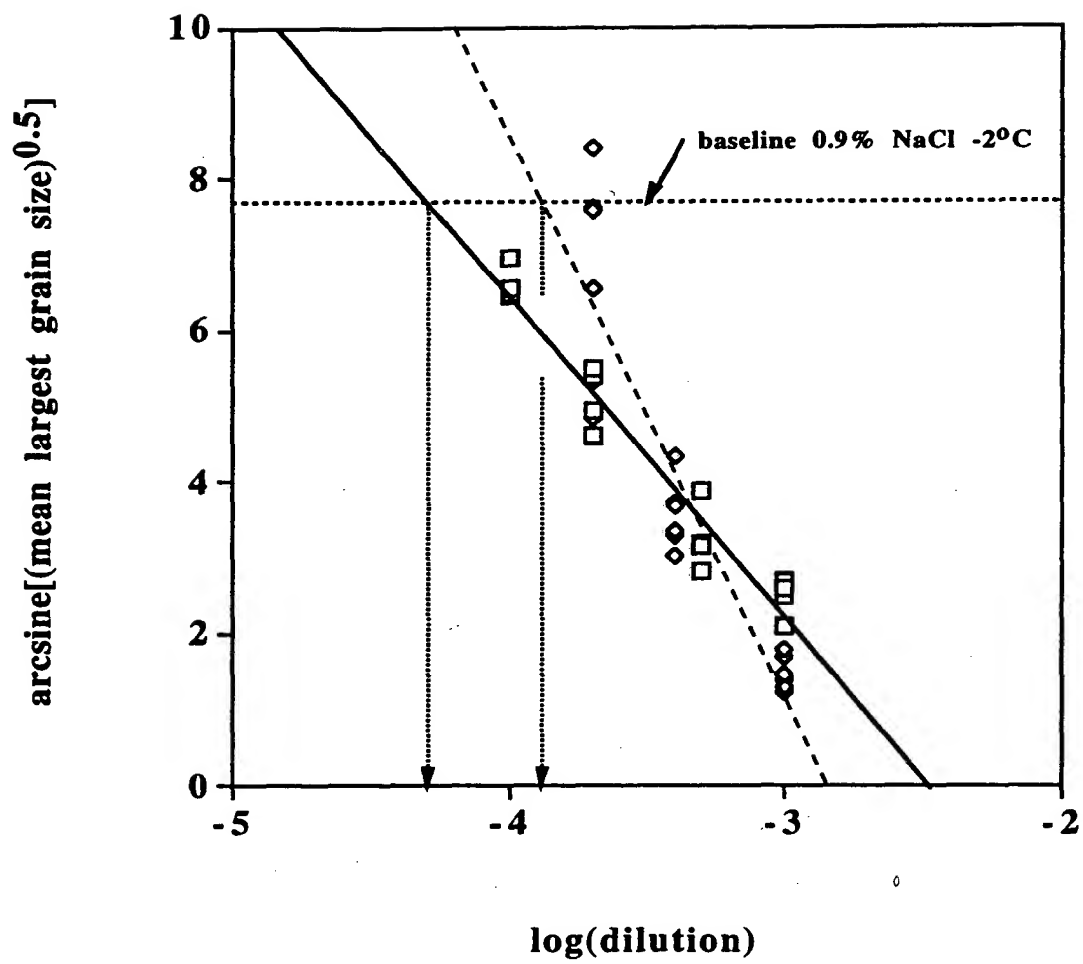


Fig. 8.29

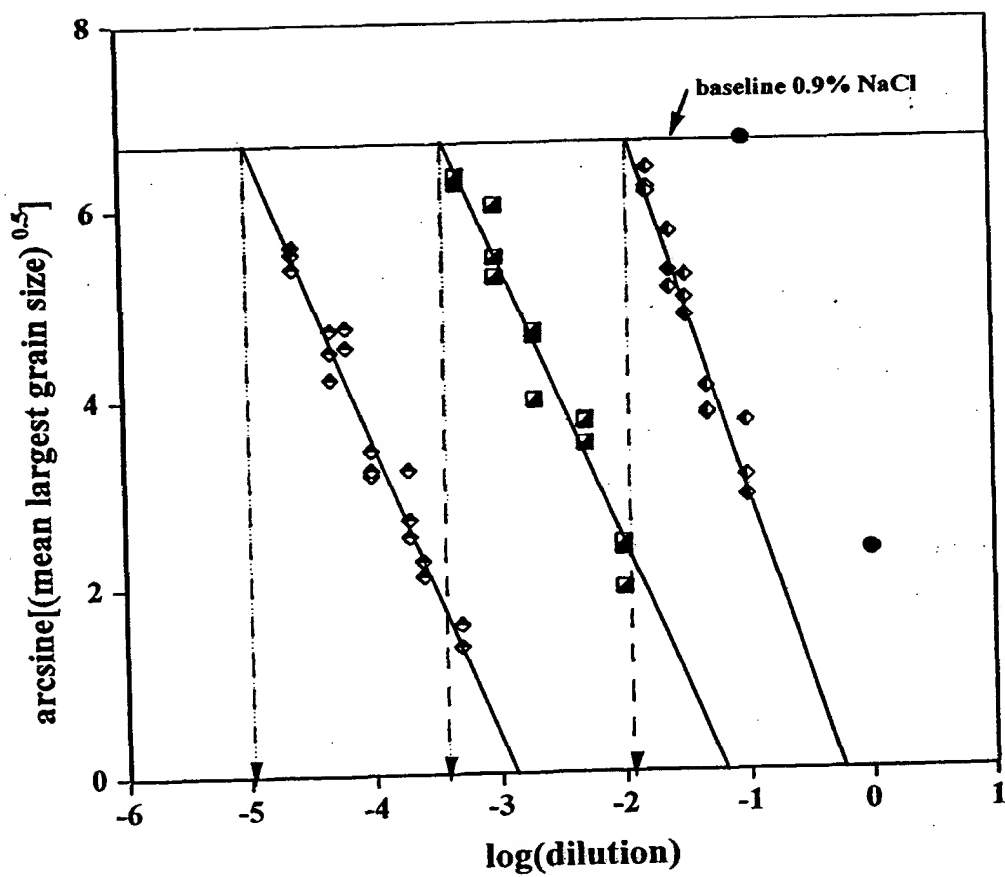


Fig. 8.30

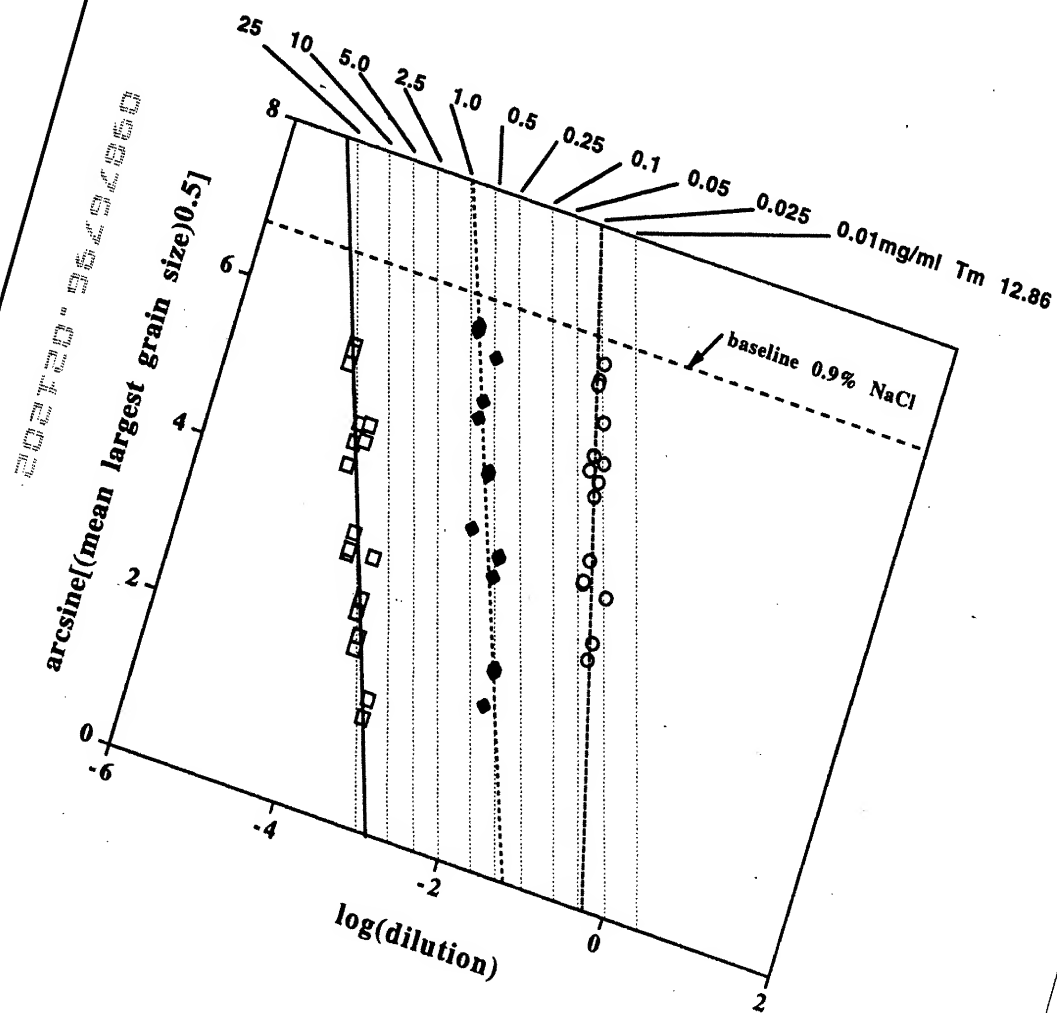
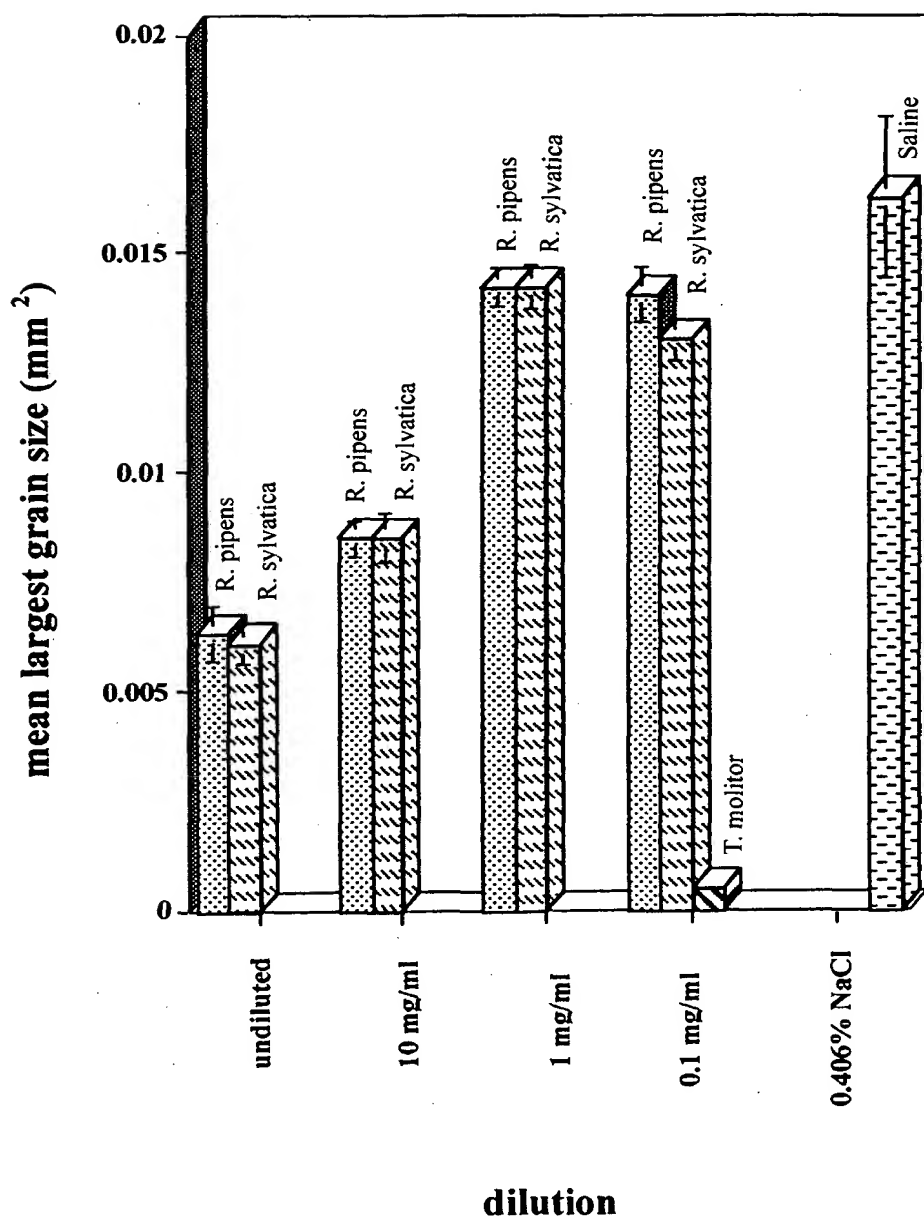


Fig. 8.31



*Fig. 8.32*

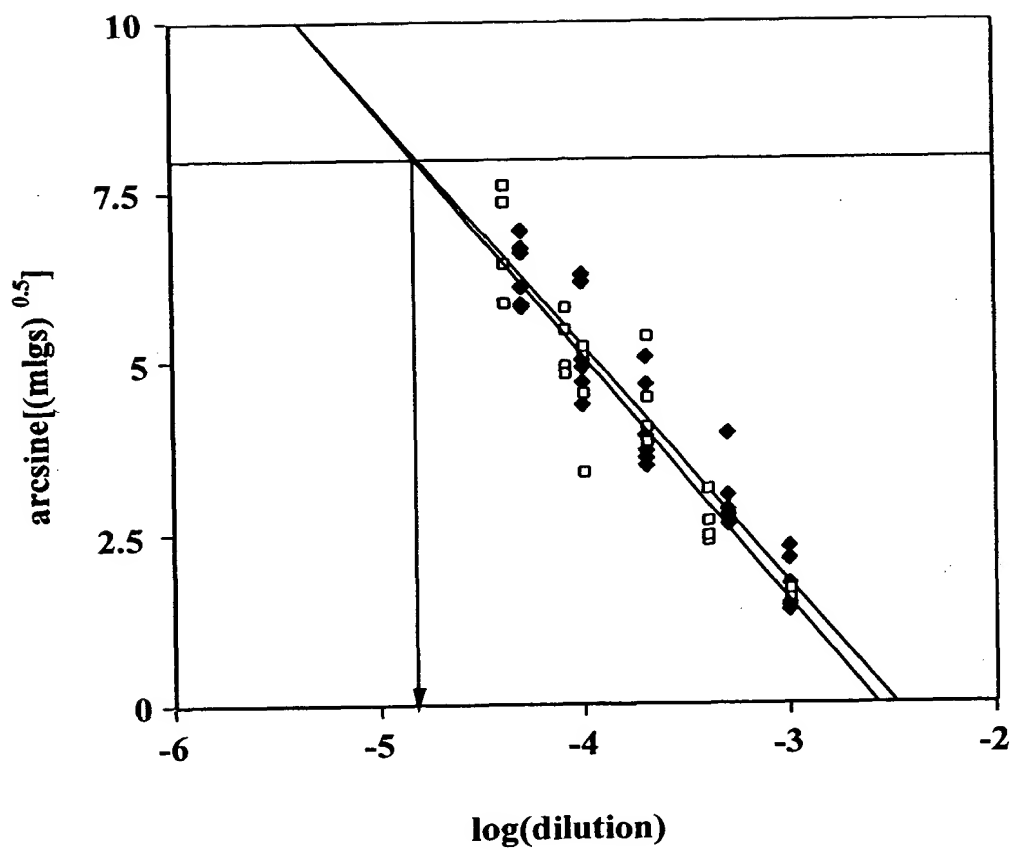


Fig. 8.33

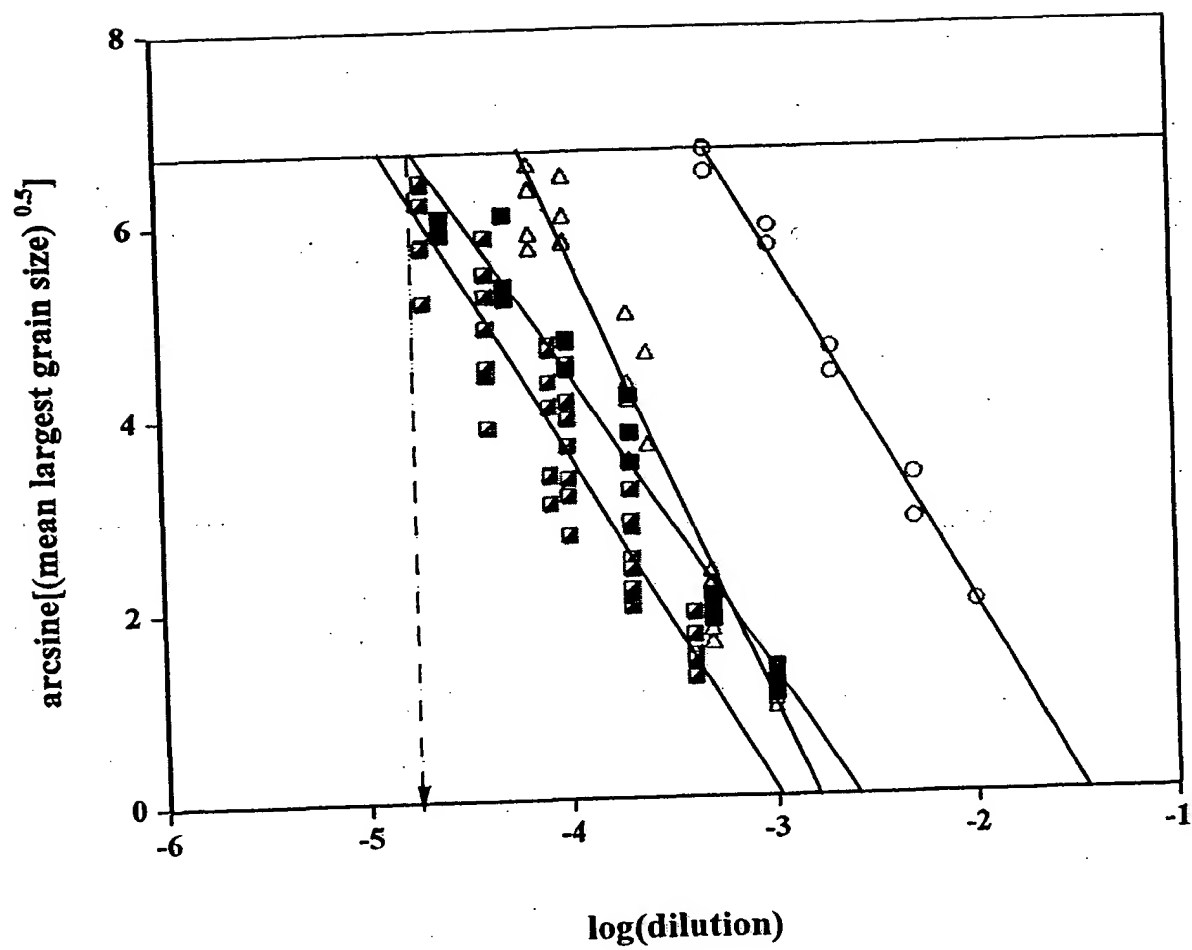


Fig. 8.34

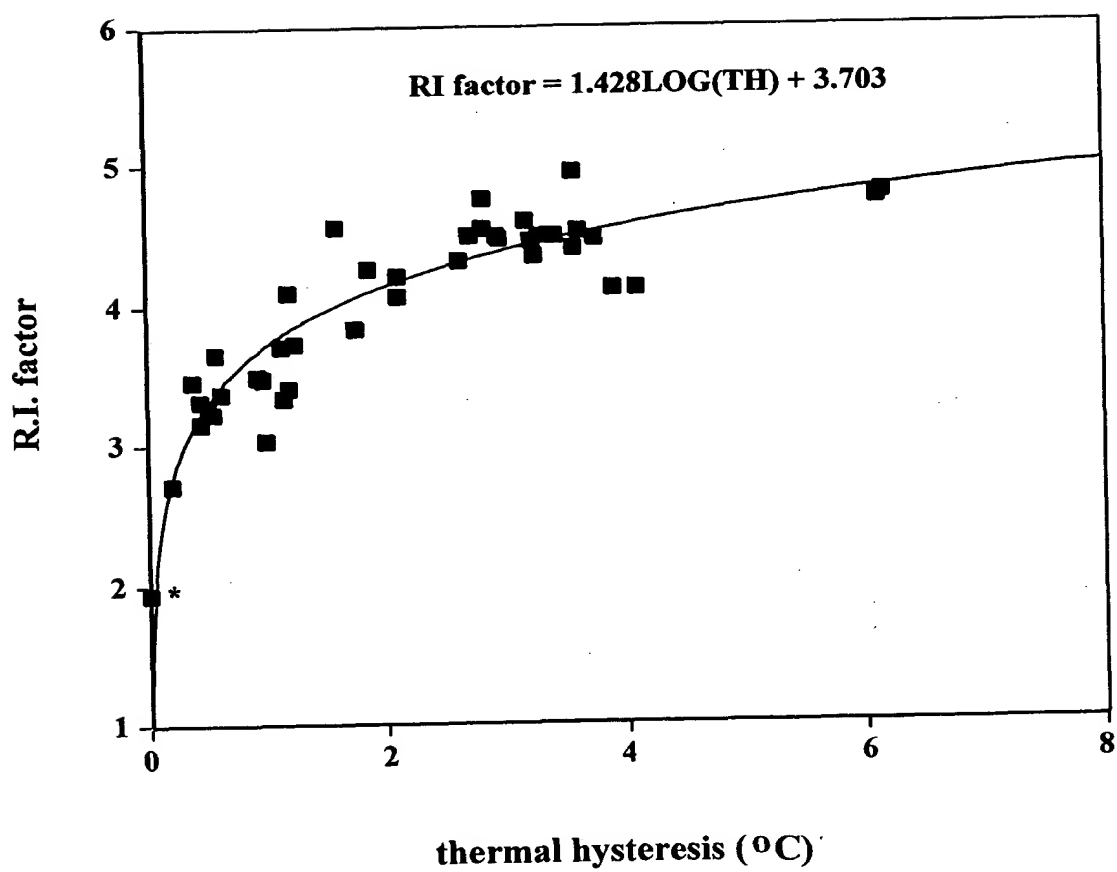


Fig. 8.35

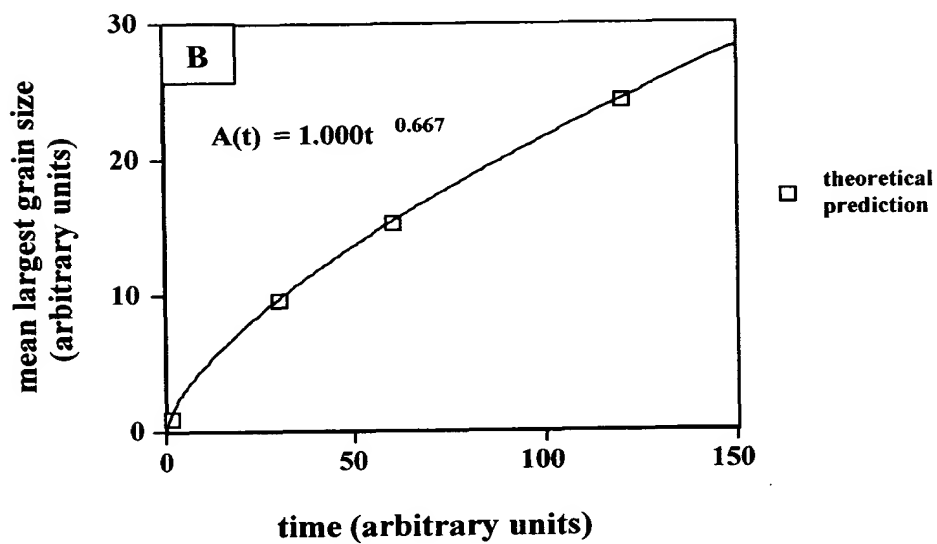
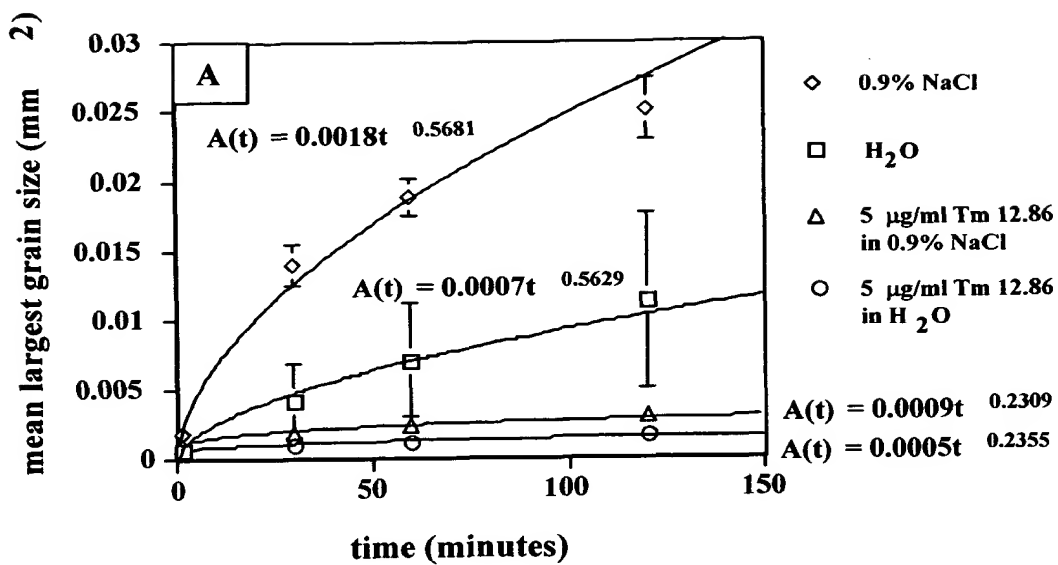


Fig. 8.36



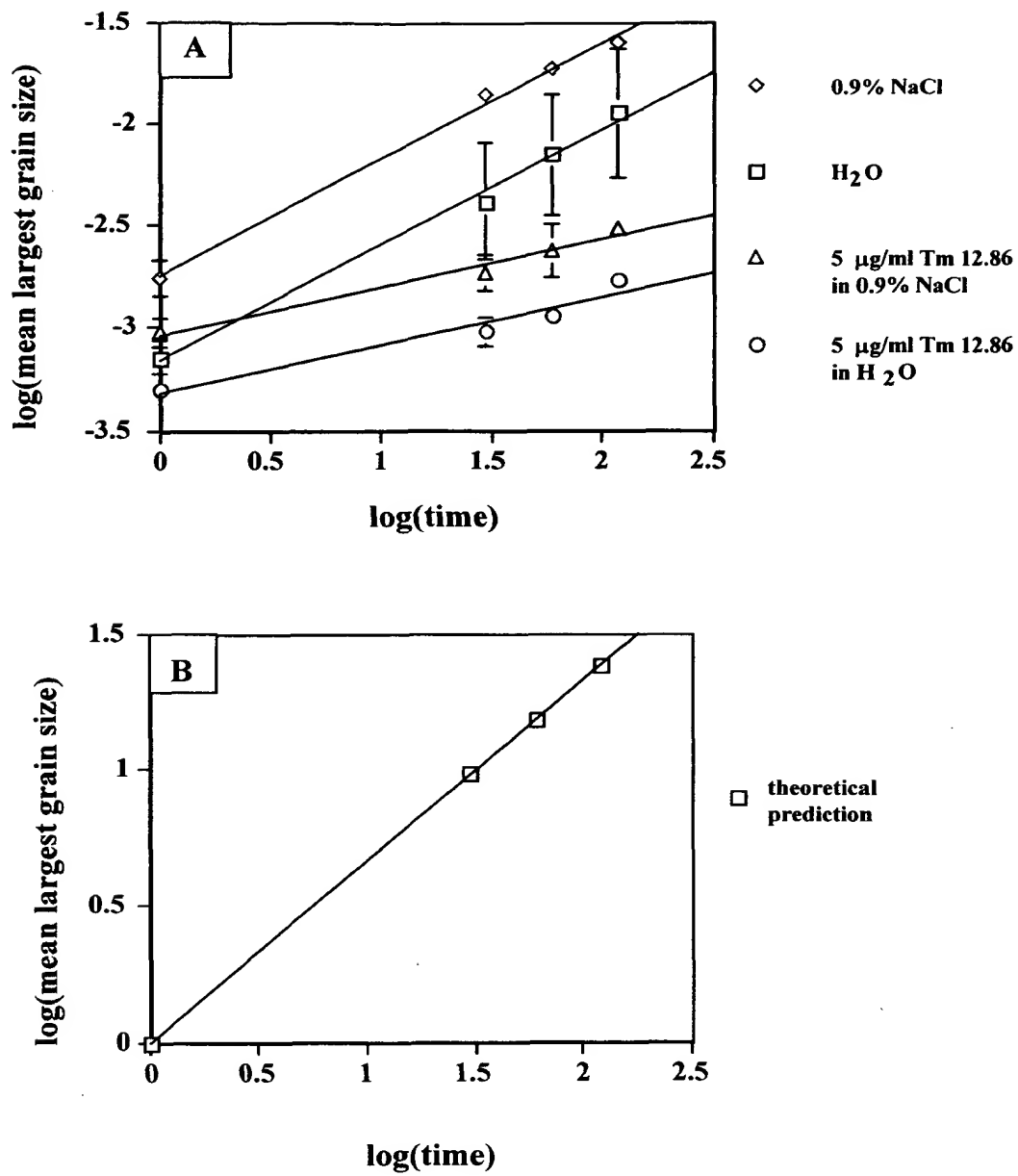
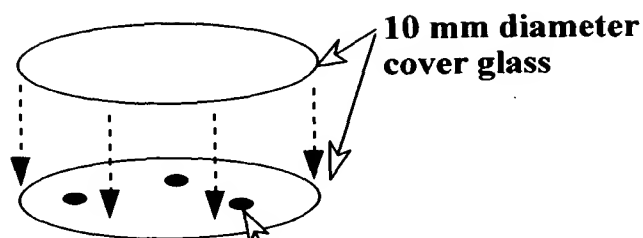


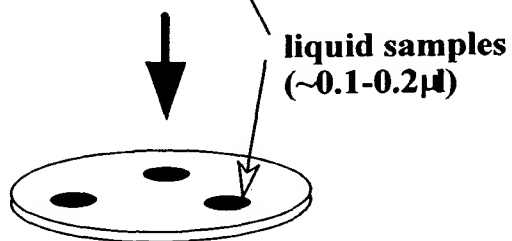
Fig. 8.37

## **"Sandwich" method of R.I. assessment**

1.



2.



3. FREEZE ON  $\sim -80$  C  
ALUMINUM PLATE ( $\sim 10$  MIN.)

4. PLACE ON COLD STAGE,  
ANNEAL AT  $-6$  C UP TO  
12+ HOURS

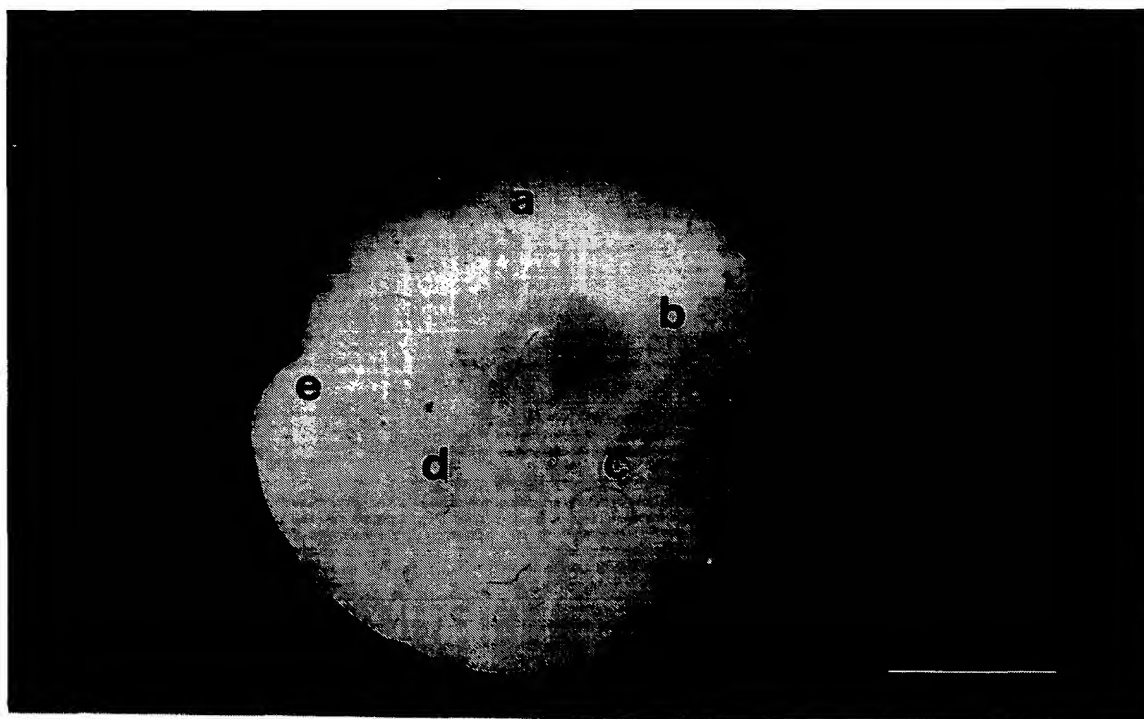
*Fig. 8.38*

**A**

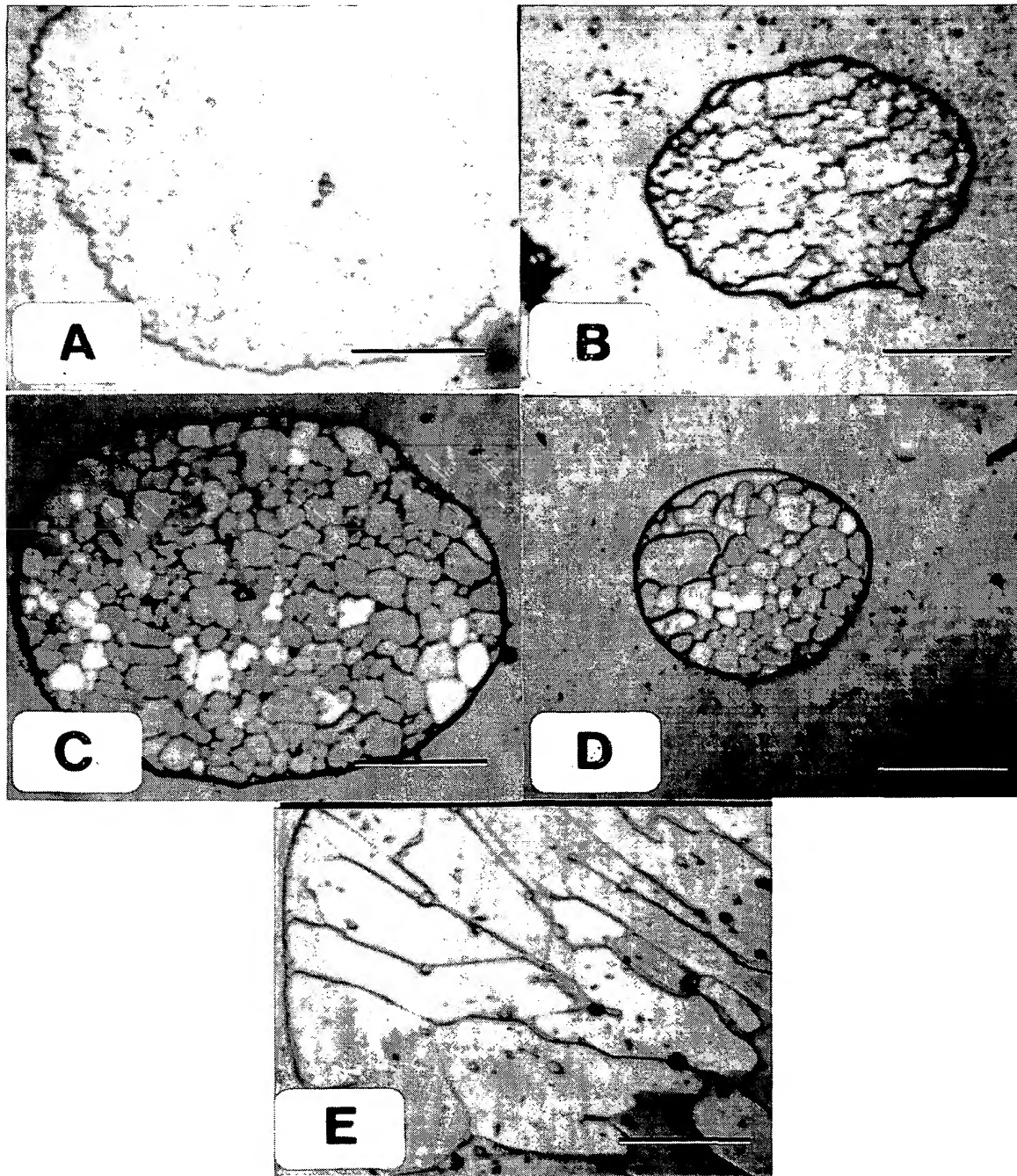
**B**

*Fig. 8.39*

09076796.024202

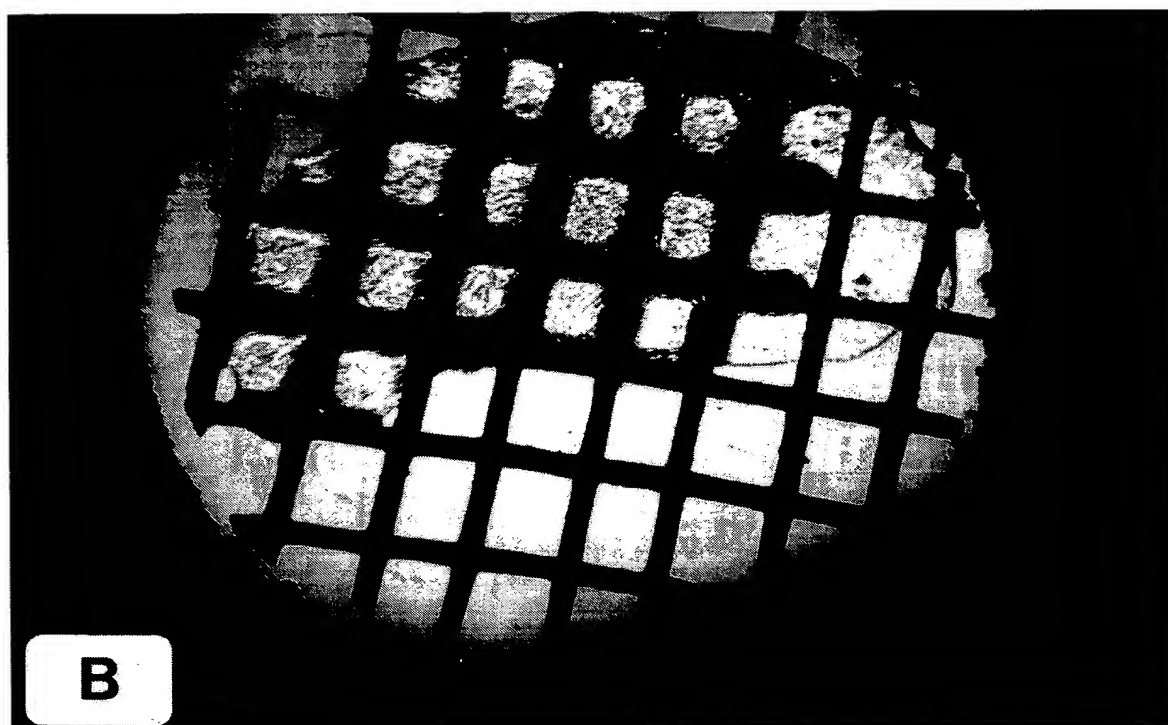
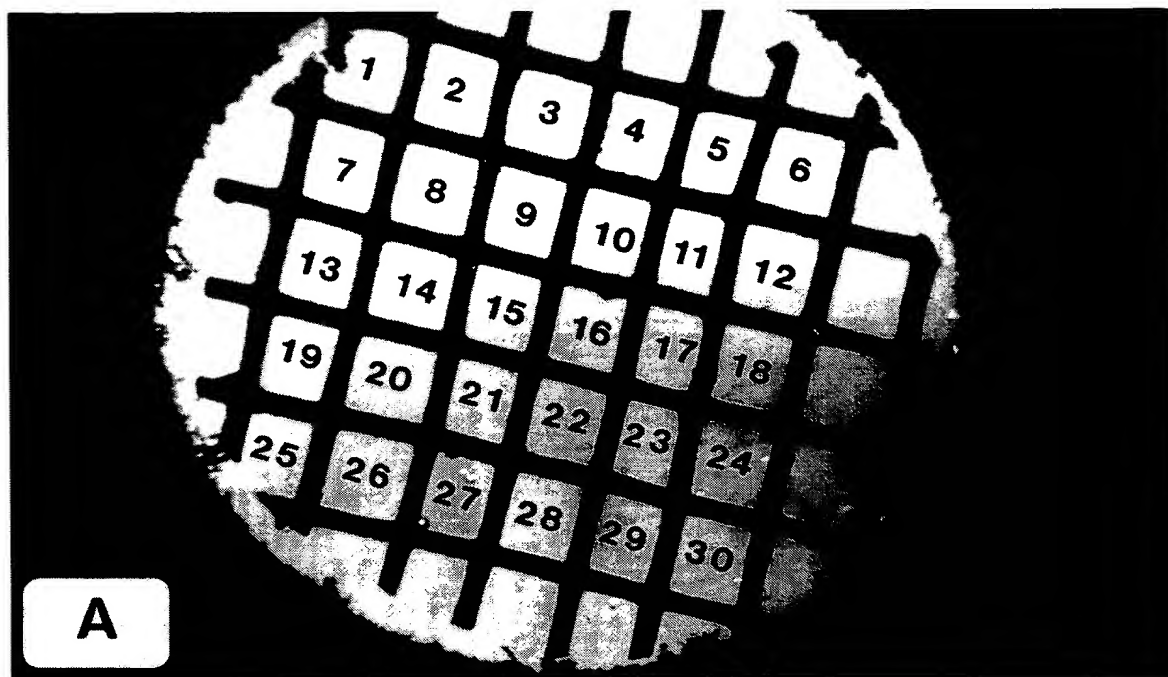


*Fig. 8.40*



*Fig. 8.41*

2025-06-26



*Fig. 8.42*

# DNA sequence of Tm 13.17 cDNA clone

B E  
 a c  
 m o  
 H R  
 I I

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT  
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA  
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAGCTC  
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA  
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA  
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACCTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCGAAGA  
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTTCATGAAAAACAAGCCAA  
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC  
 F S P V D \*

481 ATATAAAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG  
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTCCACCC

X  
 h  
 o  
 I

Fig. 8.43